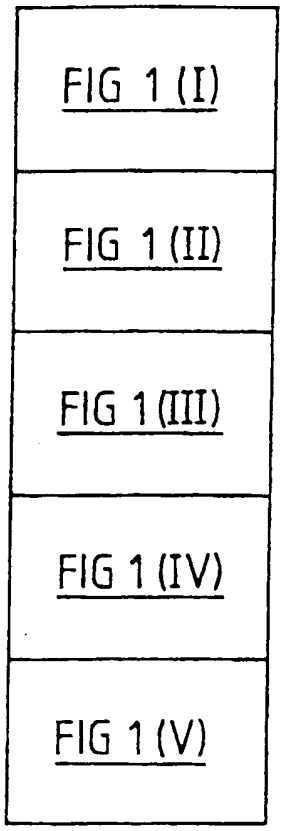


FIG 1

FIGURE 1 (I)

```
TCAGTAAACA CAGAGACTGG GGATCGATC ATG GGG CTT TGT AAG TGC CCC    50
                                Met Gly Leu Cys Lys Cys Pro
                                  1               5

AAG AGA AAG GTG ACC AAC CTG TTC TGC TTC GAA CAT CGG GTC AAC    95
Lys Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn
          10                  15                  20

GTC TGC GAG CAC TGC CTG GTA GCC AAT CAC GCC AAG TGC ATC GTC   140
Val Cys Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val
          25                  30                  35

CAG TCC TAC CTG CAA TGG CTC CAA GAT AGC GAC TAC AAC CCC AAT   185
Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn
          40                  45                  50

TGC CGC CTG TGC AAC ATA CCC CTG GCC AGC CGA GAG ACG ACC CGC   230
Cys Arg Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg
          55                  60                  65

CTT GTC TGC TAT GAT CTC TTT CAC TGG GCC TGC CTC AAT GAA CGT   275
Leu Val Cys Tyr Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg
          70                  75                  80
```

FIGURE 1 (II)

```
GCT GCC CAG CTA CCC CGA AAC ACG GCA CCT GCC GGC TAT CAG TGC  320
Ala Ala Gln Leu Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys
         85                  90                  95

CCC AGC TGC AAT GGC CCC ATC TTC CCC CCA ACC AAC CTG GCT GGC  365
Pro Ser Cys Asn Gly Pro Ile Phe Pro Pro Thr Asn Leu Ala Gly
        100                 105                 110

CCC GTG GCC TCC GCA CTG AGA GAG AAG CTG GCC ACA GTC AAC TGG  410
Pro Val Ala Ser Ala Leu Arg Glu Lys Leu Ala Thr Val Asn Trp
        115                 120                 125

GCC CGG GCA GGA CTG GGC CTC CCT CTG ATC GAT GAG GTG GTG AGC  455
Ala Arg Ala Gly Leu Gly Leu Pro Leu Ile Asp Glu Val Val Ser
        130                 135                 140

CCA GAG CCC GAG CCC CTC AAC ACG TCT GAC TTC TCT GAC TGG TCT  500
Pro Glu Pro Glu Pro Leu Asn Thr Ser Asp Phe Ser Asp Trp Ser
        145                 150                 155

AGT TTT AAT GCC AGC AGT ACC CCT GGA CCA GAG GAG GTA GAC AGC  545
Ser Phe Asn Ala Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser
        160                 165                 170
```

FIGURE 1 (III)

```
GCC TCT GCT GCC CCA GCC TTC TAC AGC CGA GCC CCC CGG CCC CCA  590
Ala Ser Ala Ala Pro Ala Phe Tyr Ser Arg Ala Pro Arg Pro Pro
        175                 180                 185

GCT TCC CCA GGC CGG CCC GAG CAG CAC ACA GTG ATC CAC ATG GGC  635
Ala Ser Pro Gly Arg Pro Glu Gln His Thr Val Ile His Met Gly
        190                 195                 200

AAT CCT GAG CCC TTG ACT CAC GCC CCT AGG AAG GTG TAT GAT ACG  680
Asn Pro Glu Pro Leu Thr His Ala Pro Arg Lys Val Tyr Asp Thr
        205                 210                 215

CGG GAT GAT GAC CGG ACA CCA GGC CTC CAT GGA GAC TGT GAC GAT  725
Arg Asp Asp Asp Arg Thr Pro Gly Leu His Gly Asp Cys Asp Asp
        220                 225                 230

GAC AAG TAC CGA CGT CGG CCG GCC TTG GGT TGG CTG GCC CGG CTG  770
Asp Lys Tyr Arg Arg Arg Pro Ala Leu Gly Trp Leu Ala Arg Leu
        235                 240                 245

CTA AGG AGC CGG GCT GGG TCT CGG AAG CGG CCG CTG ACC CTG CTC  815
Leu Arg Ser Arg Ala Gly Ser Arg Lys Arg Pro Leu Thr Leu Leu
        250                 255                 260
```

FIGURE 1 (IV)

```
CAG CGG GCG GGG CTG CTG CTA CTC TTG GGA CTG CTG GGC TTC CTG   860
Gln Arg Ala Gly Leu Leu Leu Leu Leu Gly Leu Leu Gly Phe Leu
        265                 270                 275

GCC CTC CTT GCC CTC ATG TCT CGC CTA GGC CGG GCC GCA GCT GAC   905
Ala Leu Leu Ala Leu Met Ser Arg Leu Gly Arg Ala Ala Ala Asp
        280                 285                 290

AGC GAT CCC AAC CTG GAC CCA CTC ATG AAC CCT CAC ATC CGC GTG   950
Ser Asp Pro Asn Leu Asp Pro Leu Met Asn Pro His Ile Arg Val
        295                 300                 305

GGC CCC TCC TGA GCCCCCTTGC TTGTGGCTAG GCCAGCCTAG GATGTGGGTT 1002
Gly Pro Ser  *
        310

CTGTGGAGGA GAGGCGGGGT AATGGGGAGG CTGAGGGCAC CTCTTCACTG        1052

CCCCTCTCCC TCAAGCCTAA GACACTAAGA CCCCAGACCC AAAGCCAAGT        1102

CCACCAGAGT GGCTCGCAGG CCAGGCCTGG AGTCCCCGTG GGTCAAGCAT        1152
```

FIGURE 1 (V)

```
TTGTCTTGAC TTGCTTTCTC CCGGGTCTCC AGCCTCCGAC CCCTCGCCCC      1202

ATGAAGGAGC TGGCAGGTGG AAATAAACAA CAACTTTATT                 1242
```

Figure 2

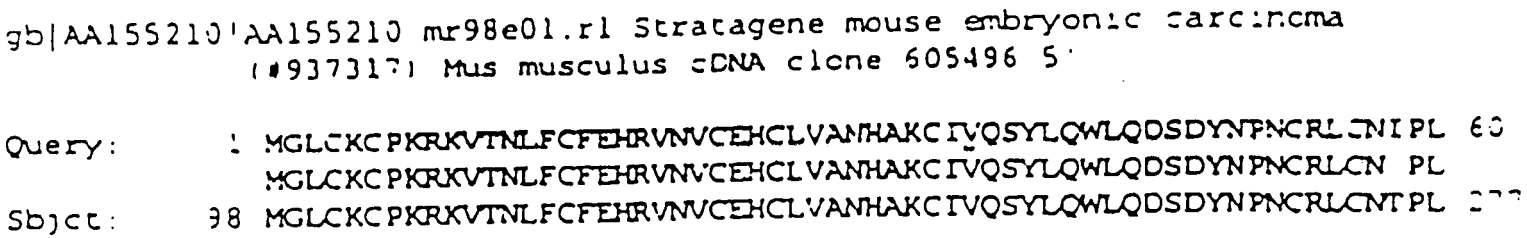


FIGURE 3

dbj|D75913| CELK111G3F C. elegans cDNA clone ykl11g3:5' end, single read.

```
Query:   7 PKRKVTNLFCFEHRVNVCEHCLVANHAKCIVQSYLQWLQDSDYNPNCRLCNIPLASRETT  66
           PKRKVTNLF +EHRVNVCE  LV NH  C+VQSYL WL D DY+PNC LC   L   +T
Sbjct:   1 PKRKVTNLFXYEHRVNVCELXLVDNHPNCVVQSYLTWLTDQDYDPNCSLCKTTLXEGDTI 180

Query:  67 RLVCYDLFHWACLNERAAQLPRNTAPAGYQCP 98    98 PSCNGPIFPPNQ  109
           RL C  L HW C +E     P  TAP GY+CP         P C+  +FPP+Q
Sbjct: 181 RLNCLHLLHWKCFDEWXGNFPDTTAPXGYRCP 276  275 PCCSQEVFPPDQ  310
```

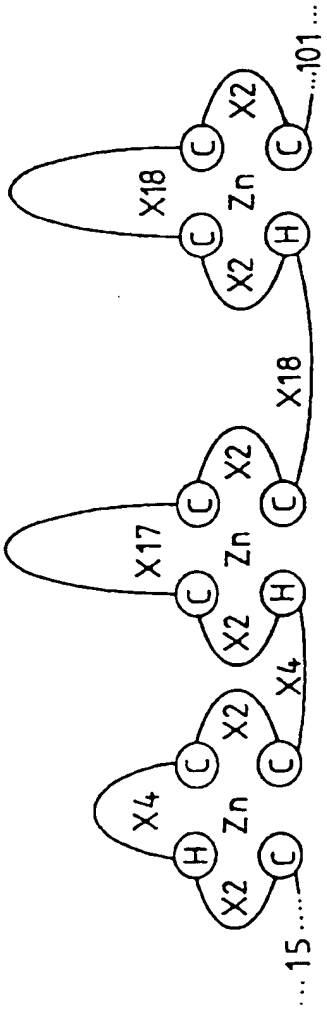


FIG 4

FIGURE 5

```
sp | P46580 |  YLBS_CAEEL HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN
                CHROMOSOME III gi|500728 (U10402) C34E10.5 gene product
                [Caenorhabditis elegans]

Query:   56    CNIPLASRETTRLVCYDLFHWACLNERAAQLPRNTAPAGYQCPSC  100
               C+I  L ++   + L C   LF W C+ E A      + + +  +CP C
Sbjct:1222     CSICLENKNPSALFCGHLFCWTCIQEHAVAATSSASTSSARCPQC 1266
```

FIGURE 6

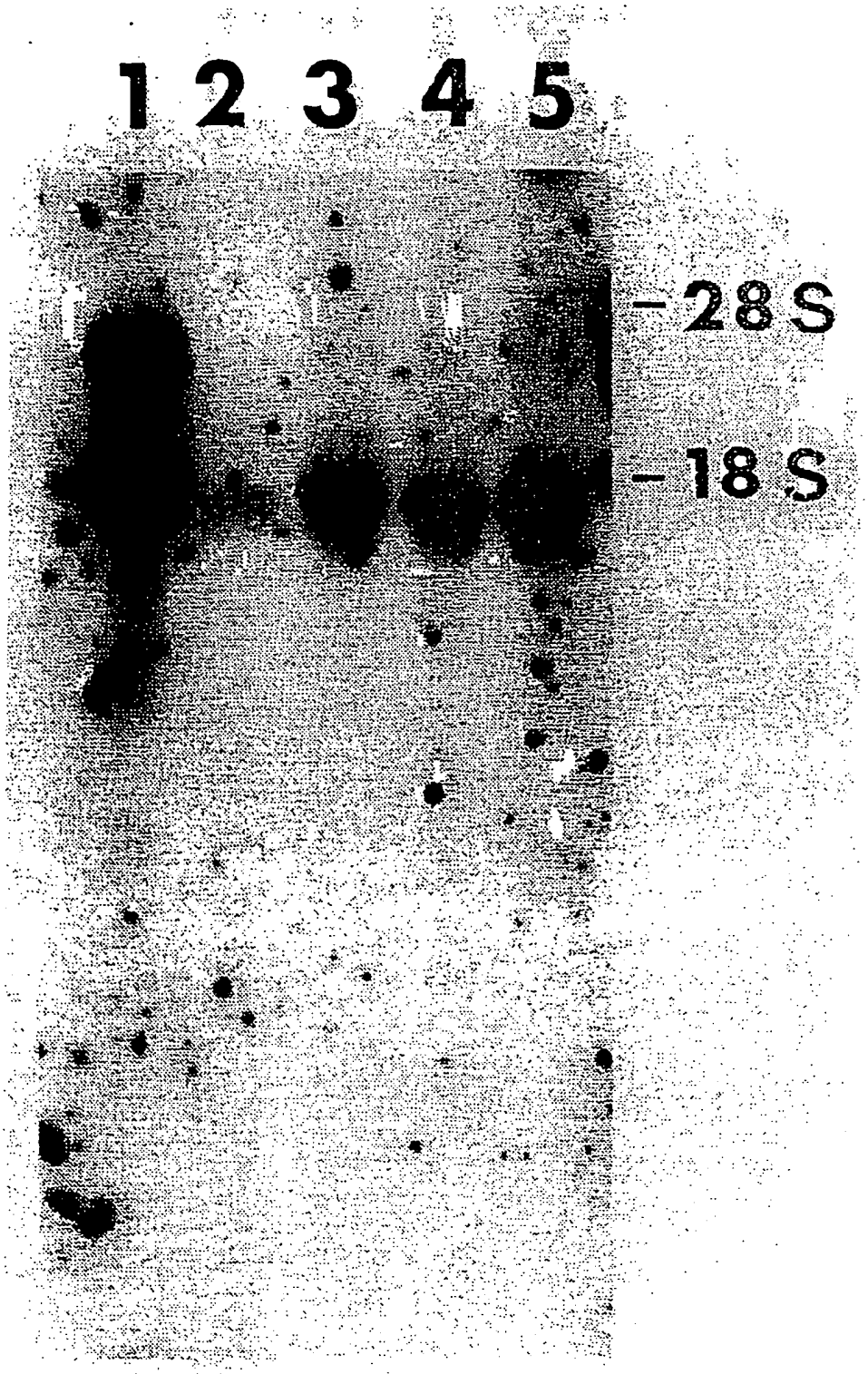
gi | 703468 | (L29051) homologous to GATA-binding transcription factor [Schizosaccharomyces pombe]

```
Query:  35  CIVQSYLQWLQDSDYNPNCRLCNI   58
            C   +  +W +D   NP C  C +
Sbjct: 175  CATTNTPKWRRDESGNPICNACGL   198

Query: 162  SSTPGPEEVDSASAAPAFYSQAPRPPASPGRPEQHTVIHMGNPEPLTHAPRKVYDTRDDD 221
            +S   PEE  S S       S  P+   SP+ +Q  +I             P +V  +  D
Sbjct: 441  ASLLNPEEPPSNSDKQPSMSNGPKSEVSPSQSQQAPLIQSSTSPVSLQFPPEVQGSNVDK 500

Query: 222  RTPGLH 227
            R   L+
Sbjct: 501  RNYALN 506
```

FIG 7



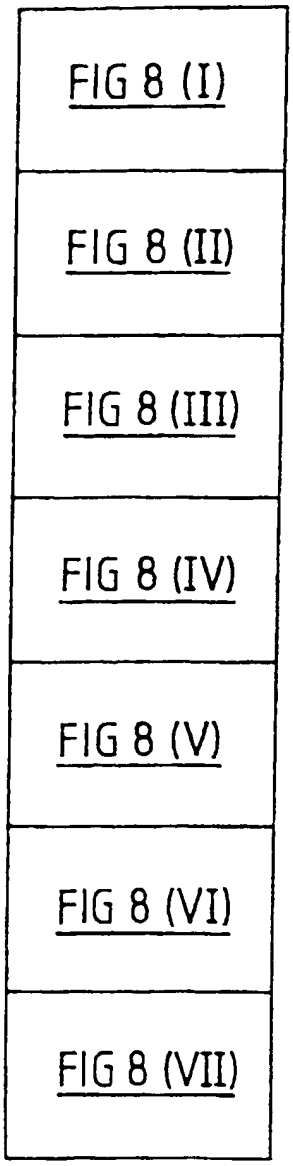


FIG 8

FIGURE 8 (I)

gb | AA074703 | AA074703 zm76g07.r1 Stratagene neuroepithelium (#937231)
Homo sapiens cDNA clone 531612 5'
Length = 417

Plus Strand HSPs:

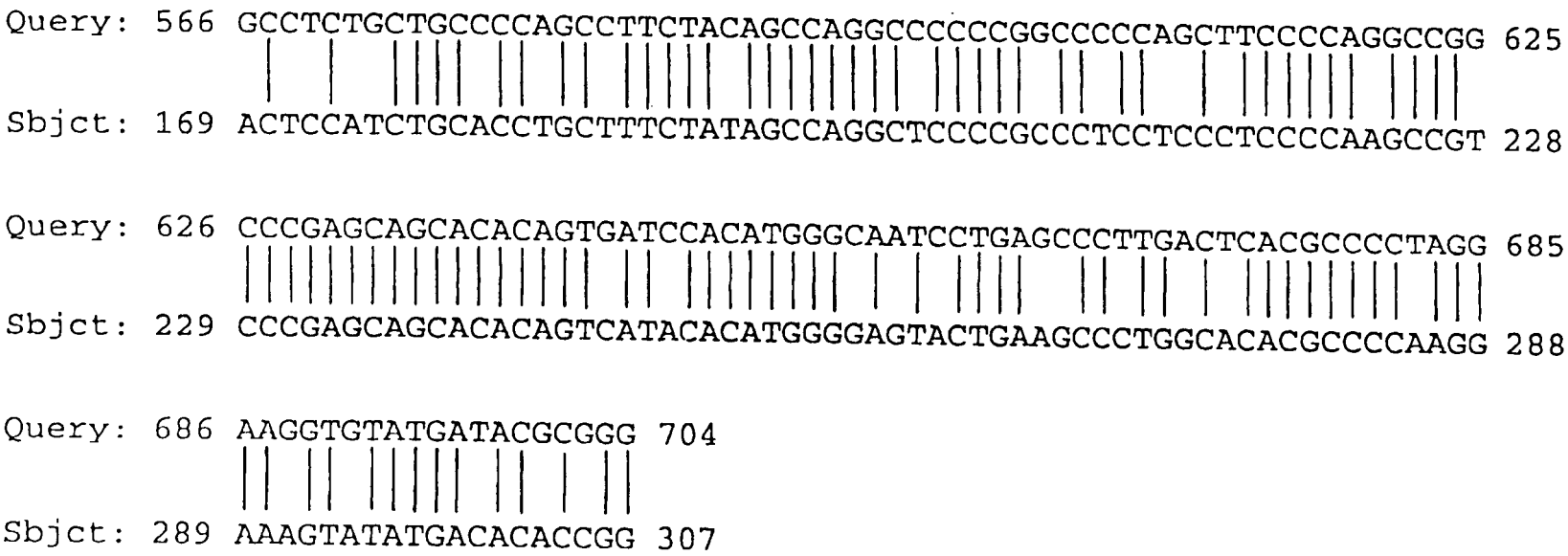
Score = 818 (226.0 bits), Expect = 6.1e-103, Sum P(5)=6.1e-103

Identities = 206/259 (79%), Positives = 206/259 (79%), Strand = Plus/Plus

```
Query: 446 GGCCTCCCTCTGATCGATGAGGTGGTGAGCCCAGAGCCCGAGCCCCTCAACACGTCTGAC 505
           || |||||||||||||||||||| | ||||||||||||||||||||||  | || |||
Sbjct:  49 GGGCTCCCTCTGATCGATGAGGTGATAAGCCCAGAGCCCGAGCCCCTCAATTCCTCAGAC 108

Query: 506 TTCTCTGACTGGTCTAGTTTTAATGCCAGCAGTACCCCTGGACCAGAGGAGGTAGACAGC 565
           |||||||| ||||| || |||||||||| ||  ||| |||  | |||||||  || ||||
Sbjct: 109 TTCTCTGATTGGTCCAGCTTTAATGCCACCACCACCTCTGTGCAAGAGGAGAGAGCCAGC 168
```

FIGURE 8(II)



Score = 230 (63.6 bits), Expect = 6.1e-103, Sum P(5)=6.1e-103
Identities = 50/55 (90%), Positives = 50/55 (90%), Strand = Plus/Plus

FIGURE 8 (III)

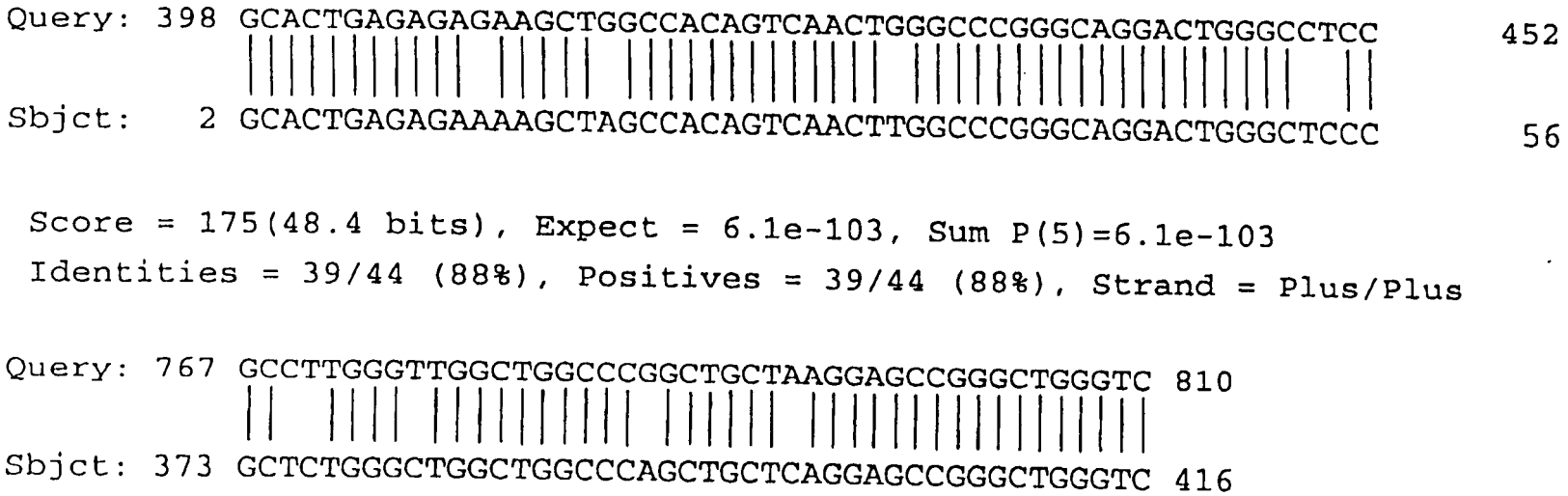


FIGURE 8 (IV)

```
Query: 731 GGAGACTGTGACGATGACAAGTACCGACGTCGGCC 765
           ||||||||||| |||||||| ||||| || |||||
Sbjct: 336 GGAGACTGTGATGATGACAAATACCGCCGCCGGCC 370
```

```
 Score = 133 (36.8 bits), Expect = 6.1e-103, Sum P(5)=5.1e-103
 Identities = 29/32 (90%), Positives = 29/32 (90%), Strand = Plus/Plus

Query: 701 CGGGATGATGACCGGACACCAGGCCTCCATGG 732
           |||||||||||||||||| ||||| | |||||
Sbjct: 305 CGGGATGATGACCGGACAGCAGGCATTCATGG 336
```

FIGURE 8 (V)

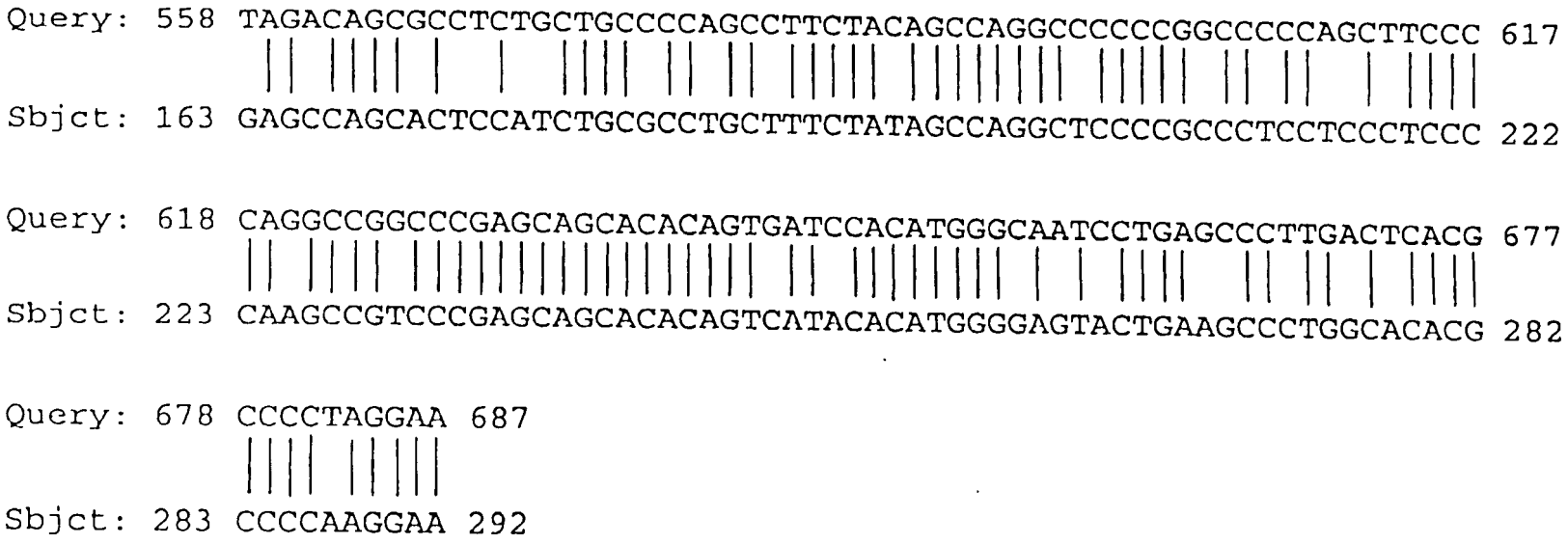
gb | AA134788 | AA134788 zm81g02.r1 Stratagene neuroepithelium (#937231)
Homo sapiens cDNA clone 532082 5'
Length = 368

Plus Strand HSPs:

Score = 563 (155.6 bits), Expect = 3.8e-87, Sum P(3)=3.8e-87
Identities = 147/190 (77%), Positives = 147/190 (77%), Strand = Plus/Plus

```
Query: 498 CGTCTGACTTCTCTGACTGGTCTAGTTTTAATGCCAGCAGTACCCCTGGACCAGAGGAGG 557
           | || |||||||||||| ||||| || |||||||||| || ||| ||| | ||||||||
Sbjct: 103 CCTCAGACTTCTCTGATTGGTCCAGCTTTAATGCCACCACCACCTCTGTGCAAGAGGAGA 162
```

FIGURE 8 (VI)



Score = 454 (125.4 bits), Expect = 3.8e-87, Sum P(3)= 3.8e-87
Identities = 94/98 (95%), Positives = 94/98 (95%), Strand = Plus/Plus

FIGURE 8 (VII)

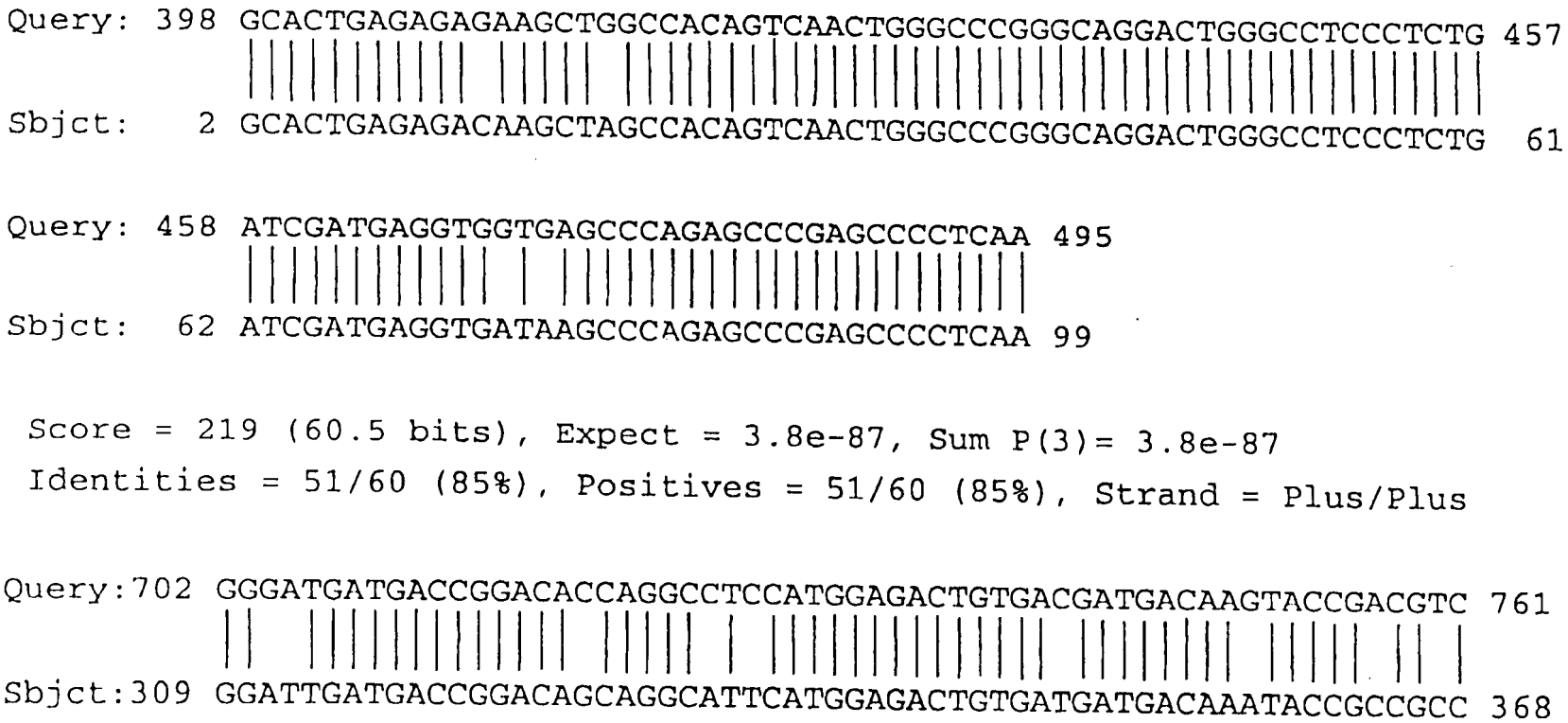


FIGURE 9

W32939 human

TACCGCCCTTCGGAACCAGTGCAGCGGCCGATCAGTAAACACAGAGACTGGGGATCGATCATGGGGCTTTGTAAG

AA242159 mouse

CTTCCGCGCTTTTCATTACCGTACGCACCGGTCA-CGATCGGCATCGCGGAGGATCGGTCATGGGACTTTGCAAG

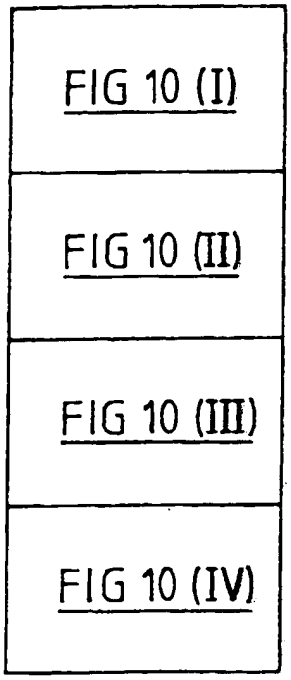


FIG 10

FIGURE 10(I)

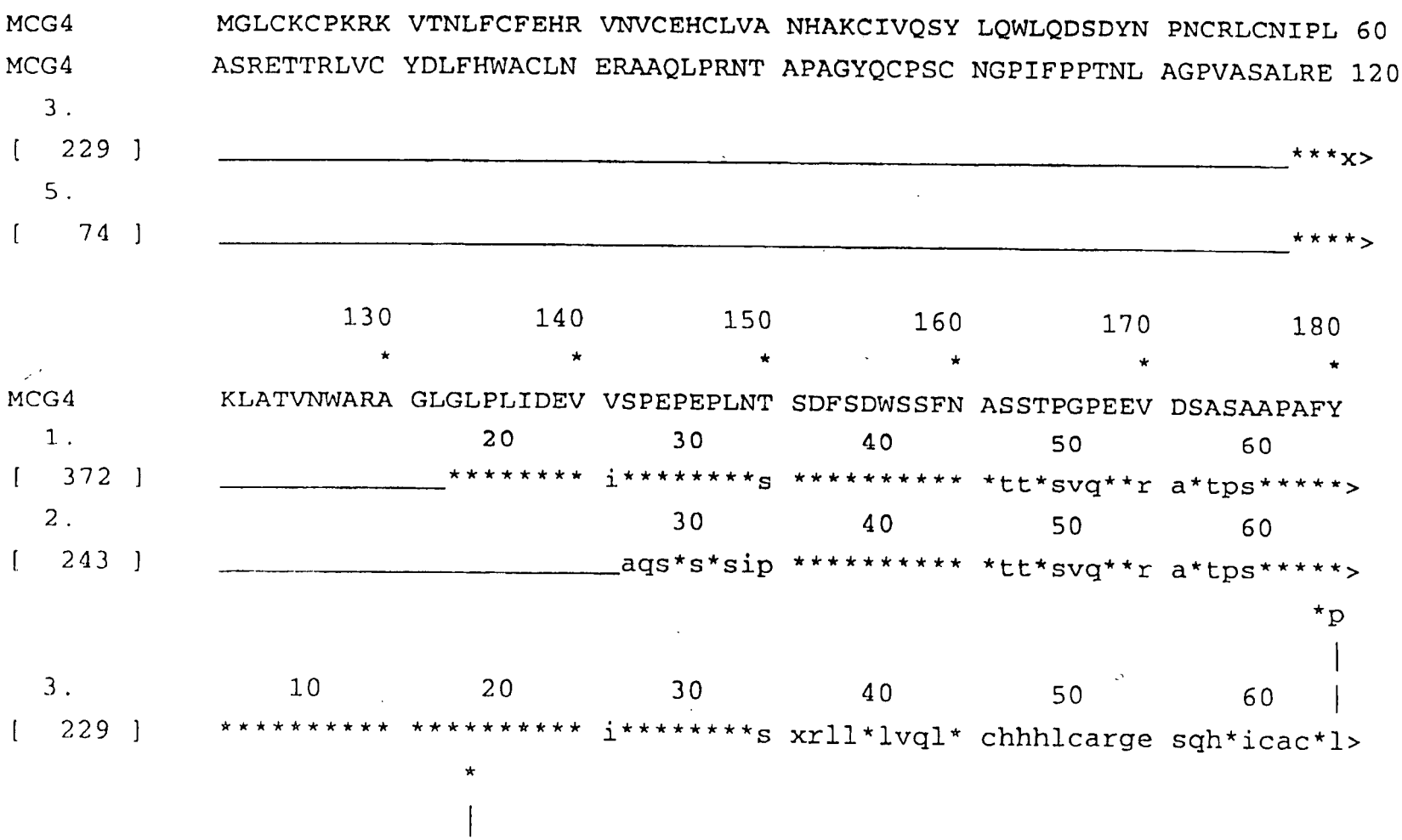

MCG4 MGLCKCPKRK VTNLFCFEHR VNVCEHCLVA NHAKCIVQSY LQWLQDSDYN PNCRLCNIPL 60
MCG4 ASRETTRLVC YDLFHWACLN ERAAQLPRNT APAGYQCPSC NGPIFPPTNL AGPVASALRE 120
3.
[229] ***x>
5.
[74] ****>
130 140 150 160 170 180
MCG4 KLATVNWARA GLGLPLIDEV VSPEPEPLNT SDFSDWSSFN ASSTPGPEEV DSASAAPAFY
1.
20 30 40 50 60
[372] ******** i********s ********** *tt*svq**r a*tps*****>
2.
30 40 50 60
[243] aqs*s*sip ********** *tt*svq**r a*tps*****>
*p
3.
10 20 30 40 50 60
[229] ********** ********** i********s xrll*lvql* chhhlcarge sqh*icac*l>

FIGURE 10 (II)

```
                          s|                                                  s
                          ||                                                  |
  5.            10        ||          30          40          50          60  |
[   74 ]    ******x*** ****smr**a q**s*-sipq tslig-pal- mppp*lckrr ep*lhlxlli>

                   190         200         210         220         230         240
                    *           *           *           *           *           *
MCG4          SRAPRPPASP GRPEQHTVIH MGNPEPLTHA PRKVYDTRDD DRTPGLHGDC DDDKYRRRPA
                                                         **
                                                         |
  1.            70          80          90          100 |  110         120
 [  372 ]    *q*****p** s********* **st*a*a** *******pgp *srhswetvm mtnt-aagl*>
  2.            70          80          90
[  243 ]    *q*****p** s********* **st*a*a** ***>
                                                        i
                                                        |
  3.          70          80          90          100 |  110         120
[  229 ]    gsp*sslpk* s*a-a*sht* gey*s*g*r- *kek*m*hg* ***a*i**** *******>
  4.          70          80          90          100         110         120
[   86 ]    __p*sslpk* s*a-a*sht* gey*s*g*rp kesi*h*gmm tgqqafm*** *********c>
                                                    h
```

FIGURE 10 (III)

```
                                                    |
  5.            70          80          90          100         110
[   74 ]    arl*allppq av*sstqsyt w*vlk*w-*t *qgk*m**** ***a*i**>
                                                    g
                                                    |
  6.                                                |100
[   38 ]    ____________________________________*t *q*******>

                     250         260         270         280         290         300
                      *           *           *           *           *           *
MCG4         LGWLARLLRS RAGSRKRPLT LLQRAGLLLL LGLLGFLALL ALMSRLGRAA ADSDPNLDPL
  1.           130
[  372 ]    *****q**** ****>
  4.
[   86 ]    s*-**>

                     310
                      *
MCG4         MNPHIRVGPS
```

FIGURE 10 (IV)

Search Analysis for Sequence: MCG4

Search from 1 to 310

Date: September 22,1997

Matrix: pam250 matrix

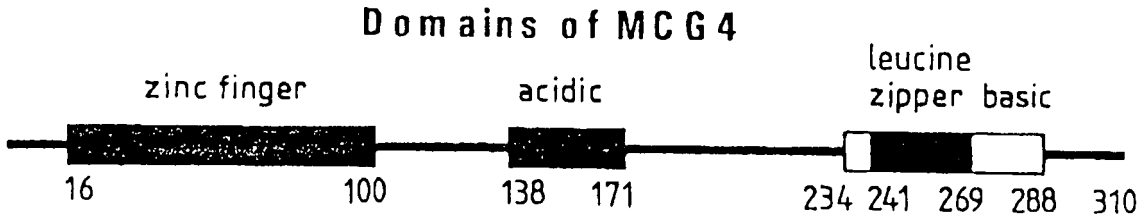
Score Region from 1 to 310

Maximum possible score: 1598

Aligned sequences:

1. = EST AA074703 phase 1 translation
2. = EST AA134788 phase 3 translation
3. = EST AA134788 phase 2 translation
4. = EST AA074703 phase 3 translation
5. = EST AA074703 phase 2 translation
6. = EST AA134788 phase 1 translation

FIGURE 11



zinc finger consensus: $CX_2HX_4CX_2CX_4HX_2CX_{17}CX_2CX_{18}HX_2CX_{18}CX_2C$

acidic domain consensus: 9/34 negatively charged amino acids, 0/34 positively charged

basic domain consensus: 13/55 positively charged amino acids, 0/55 negatively charged

leucine zipper domain consensus: $LX_6LX_6RX_6LX_6L$

alternate "novel" leucine zipper-like motif where leucine would not be aligned along the one surface of an alpha helix domain: (aa 261) $LX_6LXLX_6LXLX_6L$ (aa 286)

FIG 12 (I)	FIG 12 (II)
FIG 12 (III)	FIG 12 (IV)

FIG 12

FIG 12 (I)

Sequences producing High-scoring Segment Pairs:

gnl|PID|e236178	(Z70752 F25B3.3 [Caenorhabditis ele...
gi|1293099	(U53884) aimless RasGEF [Dictyosteli...
gi|1655941	(U67326) Ras-GRF2 [Mus musculus]
pir||s30356	CDC25 protein homolog - yeast (Cand...
sp|P43069|CC25_CANAL	CELL DIVISION CONTROL PROTEIN 25
sp|P28818|GNRP_RAT	GUANINE NUCLEOTIDE RELEASING PROTEIN...
prf||1814463A	guanine nucleotide-releasing factor ...
pir||B46199	nucleotide-exhange-factor homolog c...
gnl||PID|e238680	(X97560) hypothetical protein L1309 ...
pir||s22693	CDC25 protein homolog - mouse/gi 50...
sp|P14771|SC25_ YEAST	SCD25 PROTEIN /gi 457494 (M26647) SD...
sp|P26674|STE6_SCHPO	STE6 PROTEIN /pir s28098 ste6 prote...
pir||s28407	CDC25 protein homolog - mouse
sp|P27671|GNRP_MOUSE	GUANINE NUCLEOTIDE RELEASING PROTEIN...
gi|386047	(s62035) Ras-specific guanine nucleo...
sp|Q02342|CC25_SACKL	CELL DIVISION CONTROL PROTEIN 25 /pi...
pir||s14177	SCD25 protein - yeast (Saccharomyces...
gi|433720	(L26584) CDC25 [Homo sapiens]
gnl|PID|e241744	(Z68880) T14G10.2 [Caenorhabditis el...
gi|3484	(X03579) CDC25 protein (aa 1-1588) [...

High Score	smallest Sum Probability P(N)	N
307	3.0e-124	8
202	7.8e-22	5
152	3.6e-16	4
150	2.2e-15	3
150	2.2e-15	3
166	2.6e-15	3
166	2.6e-15	3
167	1.1e-14	1
158	3.0e-14	3
167	3.7e-14	2
158	4.6e-14	3
160	5.2e-14	2
167	1.2e-13	3
167	1.2e-13	3
153	2.0e-13	2
142	4.5e-13	2
152	5.7e-13	3
153	6.0e-13	3

FIG 12 (II)

sp|P04821|CC25_YEAST	CELL DIVISION CONTROL PROTEIN 25 /pi...
gi|915328	(U24070) Munc13-1 [Rattus norvegicus]
pir||A46199	nucleotide-exchange-factor homolog c...
pdb||1PTR|	Molecule: Protein Kinase C Delta Ty...
gi|915330	(U24071) Munc13-2 [Rattus norvegicus]
gi|474982	(D21239) 'C3G protein' [Homo sapiens...
gi|1763306	(U75361) Munc13-3 [Rattus norvegicus]
gi|806957	guanine-nucleotide exchange factor C...
sp|Q03385|GNDS_MOUSE	GUANINE NUCLEOTIDE DISSOCIATION STIM...
pir||BVBYL1	LTE1 protein - yeast (Saccharomyces...
gi|452242	(D21354) a putative guanine nucleoti...
sp|P07866|LTE1_YEAST	LOW TEMPERATURE ESSENTIAL PROTEIN /P...
gi|509050	(Z22521) protein kinase C delta [Hom...
gi|520587	(D10495) protein kinase C delta-type...
sp|P05130|KPC1_DROME	PROTEIN KINASE C, BRAIN ISOZYME (PKC...
pir||S35704	protein kinase C (EC 2.7.1.-) delta...
sp|Q05655/KPCD_HUMAN	PROTEIN KINASE C, DELTA TYPE (NPKC-D...
pir||S40279	protein kinase C mu - human /pir A5...
sp|P09215|KPCD_RAT	PROTEIN KINASE C, DELTA TYPE (NPKC-D...
gi|520878	(Z34524) serine/threonine protein ki...
gi|1519719	(U68142) RalGDS-like [Homo sapiens]

FIG 12 (III)

09/424458

FIG 12 IV

157	7.2e-13	1	
136	3.4e-12	3	
136	3.4e-12	3	
151	5.5e-12	1	
149	5.6e-12	1	
136	1.5e-11	1	
150	1.6e-11	2	
131	3.3e-11	3	
153	6.4e-11	2	
128	7.8e-11	3	
133	1.0e-10	2	
139	1.9e-10	1	
139	2.7e-10	1	
139	2.7e-10	1	
137	4.0e-10	1	
137	4.6e-10	1	
137	4.7e-10	1	
137	4.7e-10	1	
137	4.7e-10	1	
137	4.9e-10	1	
135	9.0e-10	1	
133	1.8e-09	1	
115	3.8e-09	3	

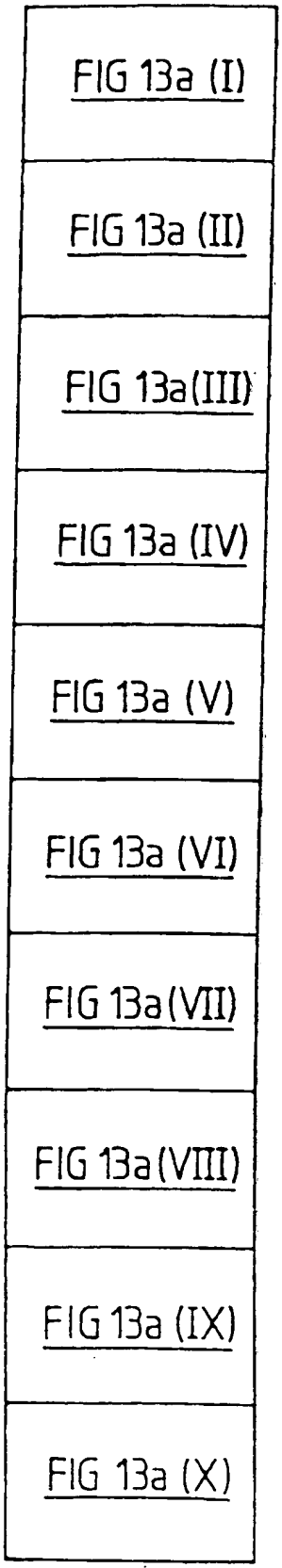


FIG 13a (I)
FIG 13a (II)
FIG 13a(III)
FIG 13a (IV)
FIG 13a (V)
FIG 13a (VI)
FIG 13a(VII)
FIG 13a(VIII)
FIG 13a (IX)
FIG 13a (X)

FIG 13a

FIGURE 13(a) (I)

```
CG ATT TCA TTC CTC GCT CCC CAC AGG TCC CTC TCC CCA AAA TAT   44
   Ile Ser Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr
     1               5                  10

TCC CAT CTT GTC CTA GCC CAT CCC CCA GAC TAT CTC AAG GAC CAG   89
Ser His Leu Val Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln
 15                  20                  25

CTG TCC CCA CGC CCC CGA CCT CCA CTA GGC CTG TGC CAC CCG CTG  134
Leu Ser Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His Pro Leu
 30                  35                  40

CCT GCA GGA AGA CGC CCG GTC CCG GGC CGG GTT AGC CCC ATG GGA  179
Pro Ala Gly Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met Gly
 45                  50                  55

ACG CAG CGC CTG TGT GGC CGC GGG ACT CAA GGC TGG CCT GGC TCA  224
Thr Gln Arg Leu Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser
 60                  65                  70

AGT GAA CAG CAC GTC CAG GAG GCG ACC TCG TCC GCG GGT TTG CAT  269
Ser Glu Gln His Val Gln Glu Ala Thr Ser Ser Ala Gly Leu His
 75                  80                  85
```

FIGURE 13(a) (II)

```
TCT GGG GTG GAC GAG CTG GGG GTT CGG TCC GAG CCC GGT GGG AGG  314
Ser Gly Val Asp Glu Leu Gly Val Arg Ser Glu Pro Gly Gly Arg
 90                  95                 100

CTC CCG GAG CGC AGC CTG GGC CCA GCC CAC CCC GCG CCG GCG GCC  359
Leu Pro Glu Arg Ser Leu Gly Pro Ala His Pro Ala Pro Ala Ala
105                 110                 115

ATG GCA GGC ACC CTG GAC CTG GAC AAG GGC TGC ACG GTG GAG GAG  404
Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu
120                 125                 130

CTG CTC CGC GGG TGC ATC GAA GCC TTC GAT GAC TCC GGG AAG GTG  449
Leu Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly Lys Val
135                 140                 145

CGG GAC CCG CAG CTG GTG CGC ATG TTC CTC ATG ATG CAC CCC TGG  494
Arg Asp Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp
150                 155                 160

TAC ATC CCC TCC TCT CAG CTG GCG GCC AAG CTG CTC CAC ATC TAC  539
Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu Leu His Ile Tyr
165                 170                 175
```

FIGURE 13(a) (III)

```
CAA CAA TCC CGG AAG GAC AAC TCC AAT TCC CTG CAG GTG AAA ACG  584
Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr
180                 185                 190

TGC CAC CTG GTC AGG TAC TGG ATC TCC GCC TTC CCA GCG GAG TTT  629
Cys His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala Glu Phe
195                 200                 205

GAC TTG AAC CCG GAG TTG GCT GAG CAG ATC AAG GAG CTG AAG GCT  674
Asp Leu Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys Ala
210                 215                 220

CTG CTA GAC CAA GAA GGG AAC CGA CGG CAC AGC AGC CTA ATC GAC  719
Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp
225                 230                 235

ATA GAC AGC GTC CCT ACC TAC AAG TGG AAG CGG CAG GTG ACT CAG  764
Ile Asp Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln
240                 245                 250

CGG AAC CCT GTG GGA CAG AAA AAG CGC AAG ATG TCC CTG TTG TTT  809
Arg Asn Pro Val Gly Gln Lys Lys Arg Lys Met Ser Leu Leu Phe
255                 260                 265
```

FIGURE 13(a) (IV)

```
GAC CAC CTG GAG CCC ATG GAG CTG GCG GAG CAT CTC ACC TAC TTG  854
Asp His Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr Leu
270                 275                 280

GAG TAT CGC TCC TTC TGC AAG ATC CTG TTT CAG GAC TAT CAC AGT  899
Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser
285                 290                 295

TTC GTG ACT CAT GGC TGC ACT GTG GAC AAC CCC GTC CTG GAG CGG  944
Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg
300                 305                 310

TTC ATC TCC CTC TTC AAC AGC GTC TCA CAG TGG GTG CAG CTC ATG  989
Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln Leu Met
315                 320                 325

ATC CTC AGC AAA CCC ACA GCC CCG CAG CGG GCC CTG GTC ATC ACA 1034
Ile Leu Ser Lys Pro Thr Ala Pro Gln Arg Ala Leu Val Ile Thr
330                 335                 340
```

FIGURE 13(a) (V)

```
CAC TTT GTC CAC GTG GCG GAG AAG CTG CTA CAG CTG CAG AAC TTC 1079
His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe
345                 350                 355

AAC ACG CTG ATG GCA GTG GTC GGG GGC CTG AGC CAC AGC TCC ATC 1124
Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile
360                 365                 370

TCC CGC CTC AAG GAG ACC CAC AGC CAC GTT AGC CCT GAG ACC ATC 1169
Ser Arg Leu Lys Glu Thr His Ser His Val Ser Pro Glu Thr Ile
375                 380                 385

AAG CTC TGG GAG GGT CTC ACG GAA CTA GTG ACG GCG ACA GGC AAC 1214
Lys Leu Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn
390                 395                 400

TAT GGC AAC TAC CGG CGT CGG CTG GCA GCC TGT GTG GGC TTC CGC 1259
Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg
405                 410                 415

TTC CCG ATC CTG GGT GTG CAC CTC AAG GAC CTG GTG GCC CTG CAG 1304
Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val Ala Leu Gln
420                 425                 430
```

FIGURE 13(a) (VI)

```
CTG GCA CTG CCT GAC TGG CTG GAC CCA GCC CGG ACC CGG CTC AAC 1349
Leu Ala Leu Pro Asp Trp Leu Asp Pro Ala Arg Thr Arg Leu Asn
435                 440                 445

GGG GCC AAG ATG AAG CAG CTC TTT AGC ATC CTG GAG GAG CTG GCC 1394
Gly Ala Lys Met Lys Gln Leu Phe Ser Ile Leu Glu Glu Leu Ala
450                 455                 460

ATG GTG ACC AGC CTG CGG CCA CCA GTA CAG GCC AAC CCC GAC CTG 1439
Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala Asn Pro Asp Leu
465                 470                 475

CTG AGC CTG CTC ACG GTG TCT CTG GAT CAG TAT CAG ACG GAG GAT 1484
Leu Ser Leu Leu Thr Val Ser Leu Asp Gln Tyr Gln Thr Glu Asp
480                 485                 490

GAG CTG TAC CAG CTG TCC CTG CAG CGG GAG CCG CGC TCC AAG TCC 1529
Glu Leu Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser Lys Ser
495                 500                 505
```

FIGURE 13(a) (VII)

```
TCG CCA ACC AGC CCC ACG AGT TGC ACC CCA CCA CCC CGG CCC CCG 1574
Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro Pro Pro Arg Pro Pro
510                 515                 520

GTA CTG GAG GAG TGG ACC TCG GCT GCC AAA CCC AAG CTG GAT CAG 1619
Val Leu Glu Glu Trp Thr Ser Ala Ala Lys Pro Lys Leu Asp Gln
525                 530                 535

GCC CTC GTG GTG GAG CAC ATC GAG AAG ATG GTG GAG TCT GTG TTC 1664
Ala Leu Val Val Glu His Ile Glu Lys Met Val Glu Ser Val Phe
540                 545                 550

CGG AAC TTT GAC GTC GAT GGG GAT GGC CAC ATC TCA CAG GAA GAA 1709
Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu
555                 560                 565

TTC CAG ATC ATC CGT GGG AAC TTC CCT TAC CTC AGC GCC TTT GGG 1754
Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe Gly
570                 575                 580

GAC CTC GAC CAG AAC CAG GAT GGC TGC ATC AGC AGG GAG GAG ATG 1799
Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met
585                 590                 595
```

FIGURE 13(a) (VIII)

```
GTT TCC TAT TTC CTG CGC TCC AGC TCT GTG TTG GGG GGG CGC ATG 1844
Val Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met
600                 605                 610

GGC TTC GTA CAC AAC TTC CAG GAG AGC AAC TCC TTG CGC CCC GTC 1889
Gly Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val
615                 620                 625

GCC TGC CGC CAC TGC AAA GCC CTG ATC CTG GGC ATC TAC AAG CAG 1934
Ala Cys Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln
630                 635                 640

GGC CTC AAA TGC CGA GCC TGT GGA GTG AAC TGC CAC AAG CAG TGC 1979
Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys
645                 650                 655

AAG GAT CGC CTG TCA GTT GAG TGT CGG CGC AGG GCC CAG AGT GTG 2024
Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val
660                 665                 670
```

FIGURE 13(a) (IX)

```
AGC CTG GAG GGG TCT GCA CCC TCA CCC TCA CCC ATG CAC AGC CAC 2069
Ser Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser His
675                 680                 685

CAT CAC CGC GCC TTC AGC TTC TCT CTG CCC CGC CCT GGC AGG CGA 2114
His His Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg
690                 695                 700

GGC TCC AGG CCT CCA GAG ATC CGT GAG GAG GAG GTA CAG ACG GTG 2159
Gly Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val
705                 710                 715

GAG GAT GGG GTG TTT GAC ATC CAC TTG TA ATAGATGCTG           2198
Glu Asp Gly Val Phe Asp Ile His Leu  *
720                 725

TGGTTGGATC AAGGACTCAT TCCTGCCTTG GAGAAAATAC TTCAACCAGA      2248

GCAGGGAGCC TGGGGGTGTC GGGGCAGGAG GCTGGGGATG GGGGTGGGAT      2293

ATGAGGGTGG CATGCAGCTG AGGGCAGGGC CAGGGCTGGT GTCCCTAAGG      2348
```


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FIGURE 13(a) (X)

TTGTACAGAC TCTTGTGAAT ATTTGTATTT TCCAGATGGA ATAAAAAGGC 2398

CCGTGTAATT AACCTTC (A)n 2416

FIGURE 13(b)

```
CGATTTCATT CCTCGCTCCC CACAGGTCCC TCTCCCCAAA ATATTCCCAT        50
CTTGTCCTAG CCCATCCCCC AGACTATCTC AAGGACCAGC TGTCCCCACG       100
CCCCCGACCT CCACTAGGCC TGTGCCACCC GCTGCCTGCA GGAAGACGCC       150
CGGTCCCGGG CCGGGTTAG CCC CAT GGG AAC GGG GTT CGG TCC GAG      196
                     *  Pro His Gly Asn Gly Val Arg Ser Glu
                           1               5
CCC GGT GGG AGG CTC CCG GAG CGC AGC CTG GGC CCA GCC CAC      238
Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro Ala His
 10                  15                  20
CCC GCG CCG GCG GCC ATG GCA GGC ACC CTG GAC CTG GAC AAG      280
Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys
     25                  30                  35
GGC TGC ACG GTG GAG GAG CT                                  300
Gly Cys Thr Val Glu Glu Leu
         40
```

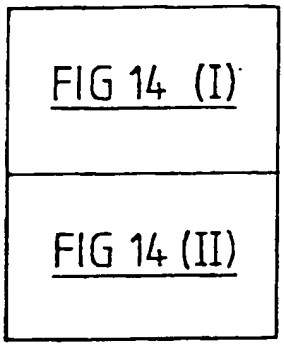


FIG 14

FIGURE 14 (I)

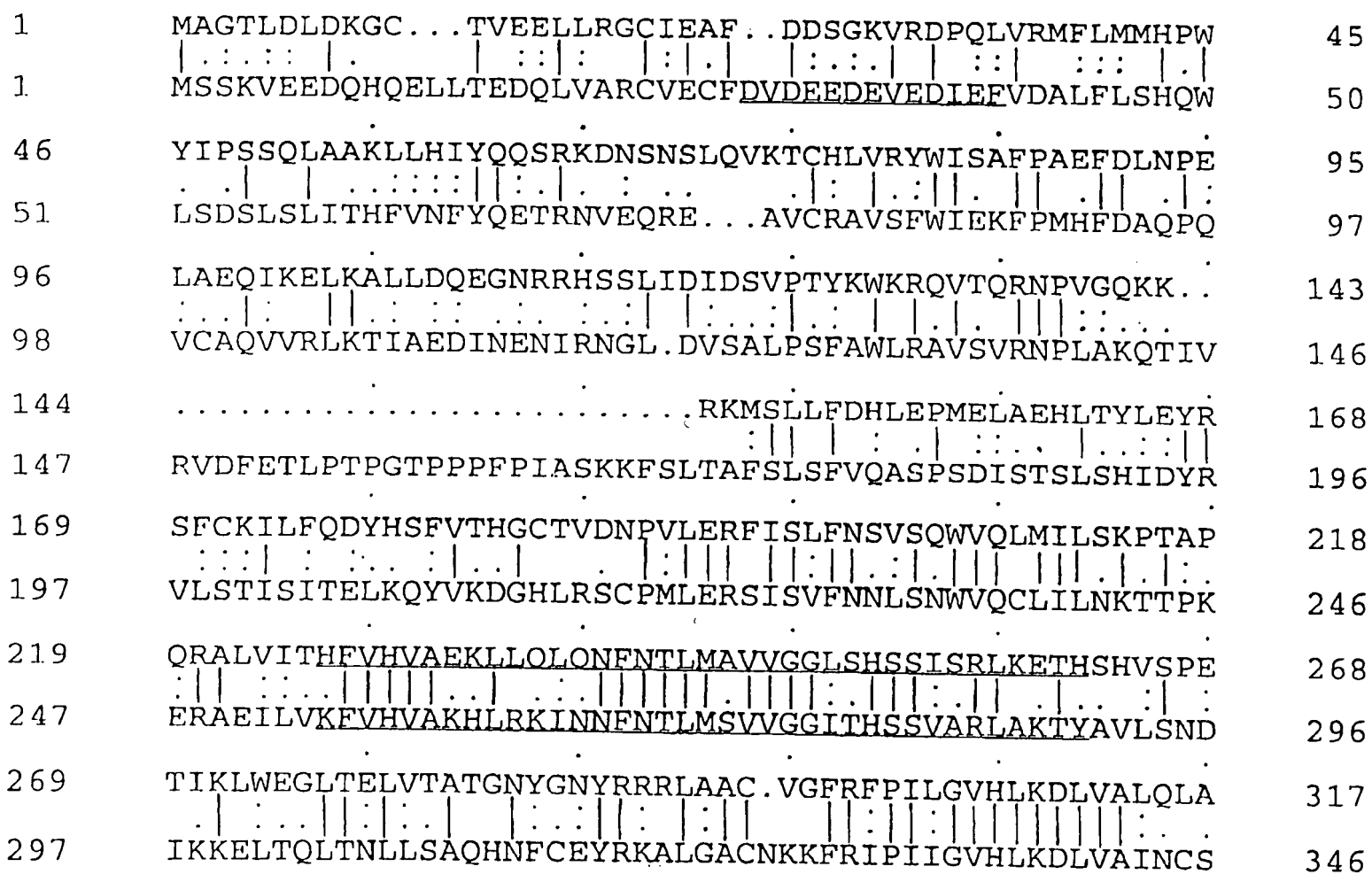

1 MAGTLDLDKGC...TVEELLRGCIEAF..DDSGKVRDPQLVRMFLMMHPW 45
1 MSSKVEEDQHQELLTEDQLVARCVECFDVDEEDEVEDIEFVDALFLSHQW 50
46 YIPSSQLAAKLLHIYQQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPE 95
51 LSDSLSLITHFVNFYQETRNVEQRE...AVCRAVSFWIEKFPMHFDAQPQ 97
96 LAEQIKELKALLDQEGNRRHSSLIDIDSVPTYKWKRQVTQRNPVGQKK.. 143
98 VCAQVVRLKTIAEDINENIRNGL.DVSALPSFAWLRAVSVRNPLAKQTIV 146
144 .....RKMSLLFDHLEPMELAEHLTYLEYR 168
147 RVDFETLPTPGTPPPFPIASKKFSLTAFSLSFVQASPSDISTSLSHIDYR 196
169 SFCKILFQDYHSFVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAP 218
197 VLSTISITELKQYVKDGHLRSCPMLERSISVFNNLSNWVQCLILNKTTPK 246
219 QRALVITHFVHVAEKLLQLQNFNTLMAVVGGLSHSSISRLKETHSHVSPE 268
247 ERAEILVKFVHVAKHLRKINNFNTLMSVVGGITHSSVARLAKTYAVLSND 296
269 TIKLWEGLTELVTATGNYGNYRRRLAAC.VGFRFPILGVHLKDLVALQLA 317
297 IKKELTQLTNLLSAQHNFCEYRKALGACNKKFRIPIIGVHLKDLVAINCS 346

FIGURE 14 (II)

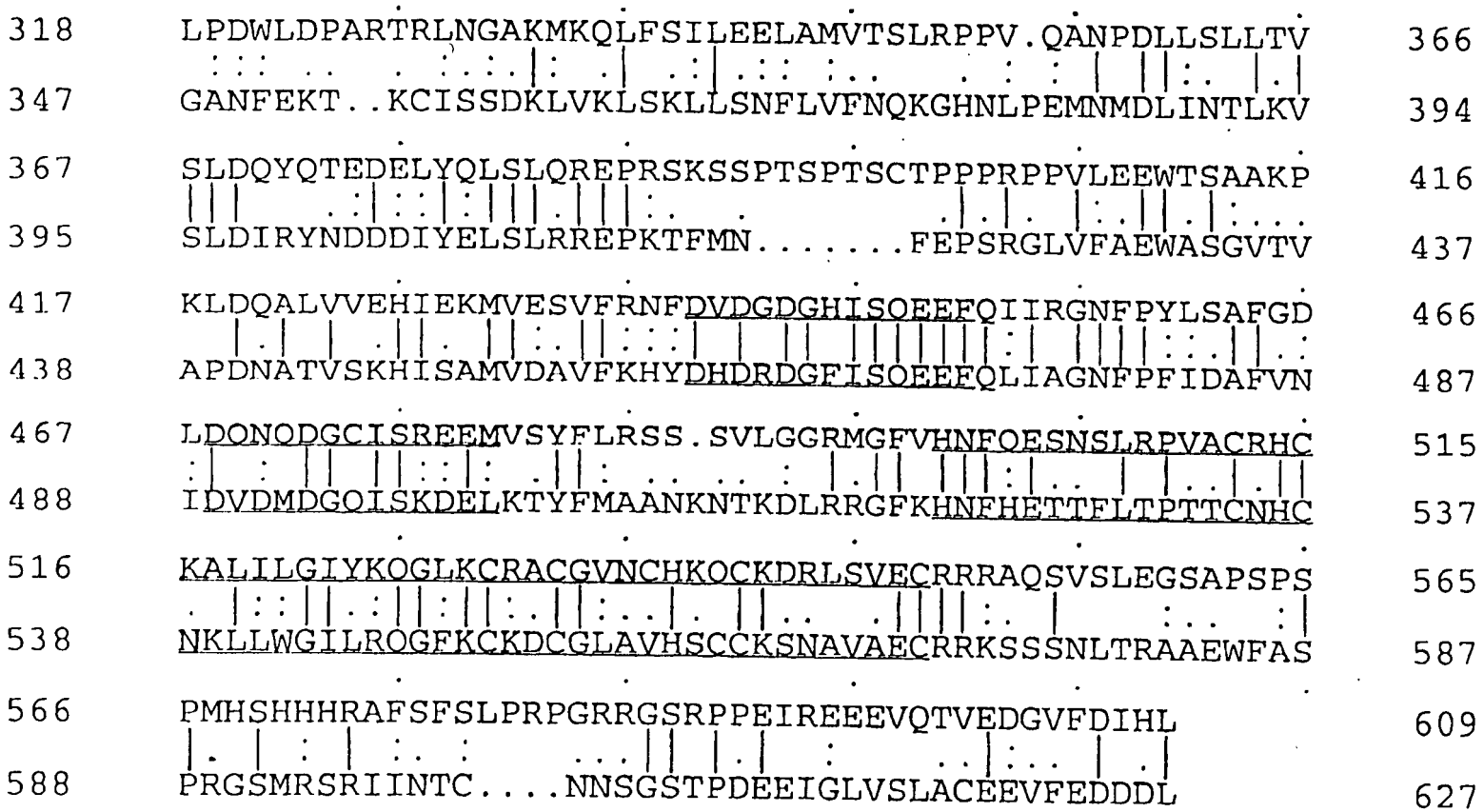


FIG 15 (I)

FIG 15 (II)

FIG 15

FIGURE 15 (I)

```
human CGATTTCATT CCTCGCTCCC CACAGGTCCC TCTCCCCAAA ATATTCCCAT CTTGTCCTAG  60
human CCCATCCCCC AGACTATCTC AAGGACCAGC TGTCCCCACG CCCCCGACCT CCACTAGGCC 120
human TGTGCCACCC GCTGCCTGCA GGAAGACGCC CGGTCCCGGG CCGGGTTAGC CCCATGGGAA 180
human CGCAGCGCCT GTGTGGCCGC GGGACTCAAG GCTGGCCTGG CTCAAGTGAA CAGCACGTCC 240
mouse                                ***tcag** ****ag**** t********* ***a*g***t>
human AGGAGGCGAC CTCGTCCGCG GGTTTGCATT CTGGGGTGGA CGAGCTGGGG GTTCGGTCCG 300
                                                          acagg
mouse g*****t**a **-*catt** ********** ***aa**aa* g**ct***** **a**aat**>
human AGCCCGGTGG GAGGCTCCCG GAGCGCAGCC TGGGCCCAGC CCACCCCGCG CCGGCGGCCA 360
mouse ***a*t**** *******tga ***t*t*a*t ****t*t*** ***-*tg**a *****a****>
human TGGCAGGCAC CCTGGACCTG GACAAGGGCT GCACGGTGGA GGAGCTGCTC CGCGGGTGCA 420
mouse ****ga**** t********* ********t* ****c***** ********** **t**c**t*>
human TCGAAGCCTT CGATGACTCC GGGAAGGTGC GGGACCCGCA GCTGGTGCGC ATGTTCCTCA 480
```

FIGURE 15 (II)

```
mouse ********** t********t **a******* *a**t**a** ***a****** *****t****>
human TGATGCACCC CTGGTACATC CCCTCCTCTC AGCTGGCGGC CAAGCTGCTC CACATCTACC 540
mouse ********** *********a **t******* *******tt* g**a****** ***t****t*>
human AACAATCCCG GAAGGACAAC TCCAATTCCC TGCAGGTGAA AACGTGCCAC CTGGTCAGGT 600
mouse *g******** ********** ********t* *a***a**** ******t*** t*********>
human ACTGGATCTC CGCCTTCCCA GCGGAGTTTG ACTTGAACCC GGAGTTGGCT GAGCAGATCA 660
mouse ********** a********* **a*****c* ********** a***c***** **a*******>
human AGGAGCTGAA GGCTCTGCTA GACCAAGAAG GGAACCGACG GCACAGCAGC CTAATCGACA 720
mouse ********** *******t** ********** *******ca* ********** **c*******>
human TAGACAGCGT
                                                                      730
mouse *c**g**t**
```

Substitute Sheet (Rule 26)

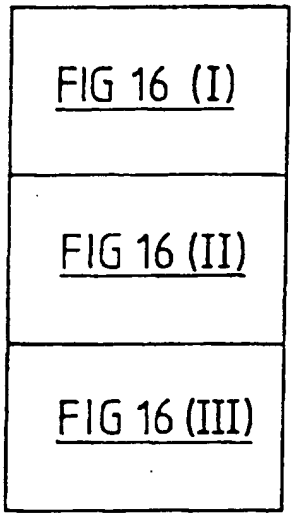


FIG 16

FIGURE 16 (I)

```
CACGCCTCGG AAGGGAGGTT TGGGGTCGGT GGTTTCACAG TGAGTGTGTC          50
TGAAGCCAAA TGGTCGGAAA CCGTTACCCG CTCTCCTAG GCC CGG CTA          98
                                          *  Ala Arg Leu
                                             1
GTG GGG ACC CCA ACC GCC TGC GGC TGC CCC TCC CAA GTT CCT         140
Val Gly Thr Pro Thr Ala Cys Gly Cys Pro Ser Gln Val Pro
      5                  10                  15

CCC TGT TGG CCA GGC ATC CAG GTC TCC AGT CTC CGA GCT GCG         182
Pro Cys Trp Pro Gly Ile Gln Val Ser Ser Leu Arg Ala Ala
          20                  25                  30

GAG AAC CCA CCG CCA CAT GCG GCT GCC CCT TTC CAT TCG ACC         224
Glu Asn Pro Pro Pro His Ala Ala Ala Pro Phe His Ser Thr
              35                  40                  45

CTG TGG GGA GCC AGG CTT CCG GGG CCC CGT TCC TCC TGT GTG         266
Leu Trp Gly Ala Arg Leu Pro Gly Pro Arg Ser Ser Cys Val
                  50                  55

AAC TGG GCC CCC CGC CCC CAT TCC CAG ACA TCA AGG CCG CGT         308
Asn Trp Ala Pro Arg Pro His Ser Gln Thr Ser Arg Pro Arg
 60                  65                  70
```

FIGURE 16 (II)

```
CTC CAG ATA GCC ACG ATT TCA TTC CTC GCT CCC CAC AGG TCC          350
Leu Gln Ile Ala Thr Ile Ser Phe Leu Ala Pro His Arg Ser
     75                  80                  85

CTC TCC CCA AAA TAT TCC CAT CTT GTC CTA GCC CAT CCC CCA          392
Leu Ser Pro Lys Tyr Ser His Leu Val Leu Ala His Pro Pro
          90                  95                 100

GAC TAT CTC AAG GAC CAG CTG TCC CCA CGC CCC CGA CCT CCA          434
Asp Tyr Leu Lys Asp Gln Leu Ser Pro Arg Pro Arg Pro Pro
              105                 110                 115

CTA GGC CTG TGC CAC CCG CTG CCT GCA GGA AGA CGC CCG GTC          476
Leu Gly Leu Cys His Pro Leu Pro Ala Gly Arg Arg Pro Val
                  120                 125

CCG GGC CGG GTT AGC CCC ATG GGA ACG CAG CGC CTG TGT GGC          518
                    *  Pro His Gly Asn
Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu Cys Gly
130                 135                 140
```

FIGURE 16 (III)

```
CGC GGG ACT CAA GGC TGG CCT GGC TCA AGT GAA CAG CAC GTC          560
Arg Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val
    145                 150                 155

CAG GAG GCG ACC TCG TCC GCG GGT TTG CAT TCT GGG GTG GAC          602
Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp
        155                 160                 165

GAG CTG GGG GTT CGG TCC GAG CCC GGT GGG AGG CTC CCG GAG          644
Glu Leu Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu
            170                 175                 180

CGC AGC CTG GGC CCA GCC CAC CCC GCG CCG GCG GCC ATG GCA          686
Arg Ser Leu Gly Pro Ala His Pro Ala Pro Ala Ala Met Ala
                185                 190

GGC ACC CTG GAC CTG GAC AAG GGC TGC ACG GTG G                    720
Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr Val
195                 200                 205
```

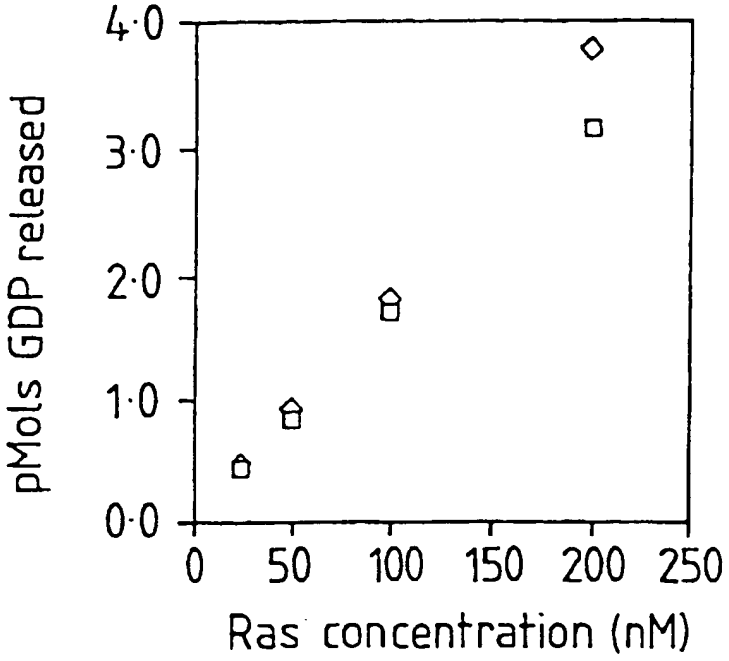
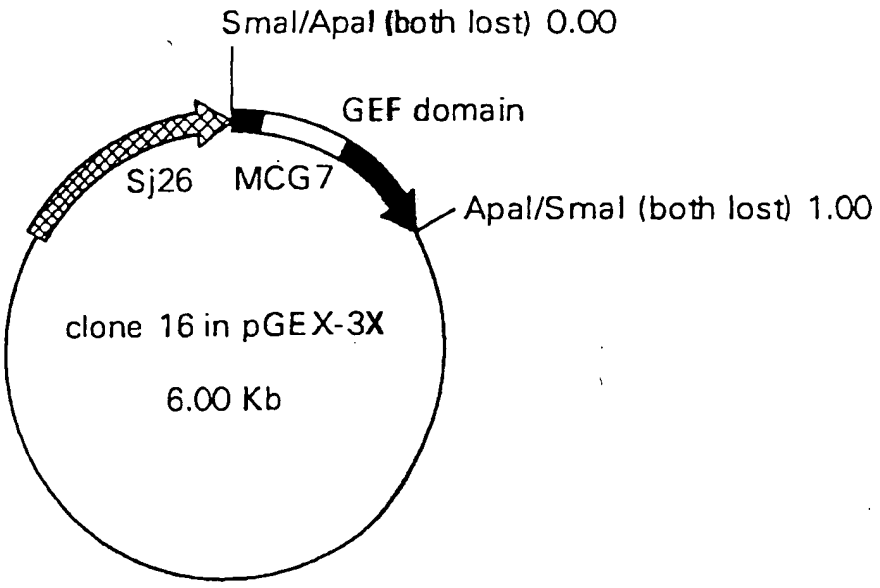

4·0
3·0
2·0
1·0
0·0
pMols GDP released
0
50
100
150
200
250
Ras concentration (nM)

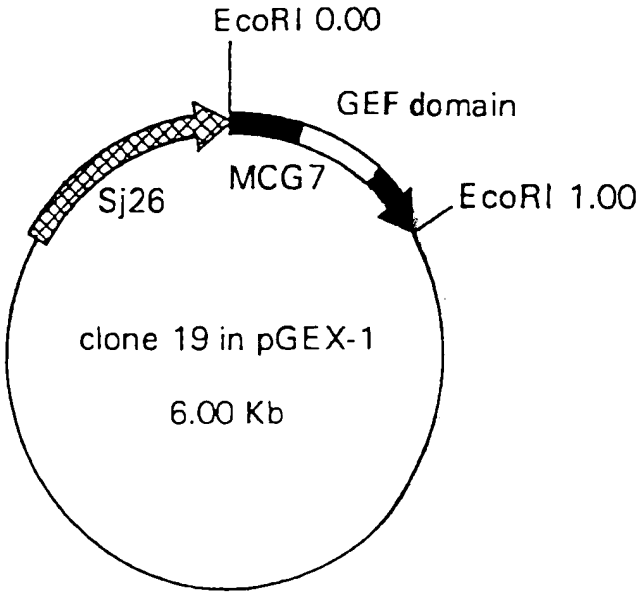
FIGURE 17

FIGURE 18 (Cont. I)



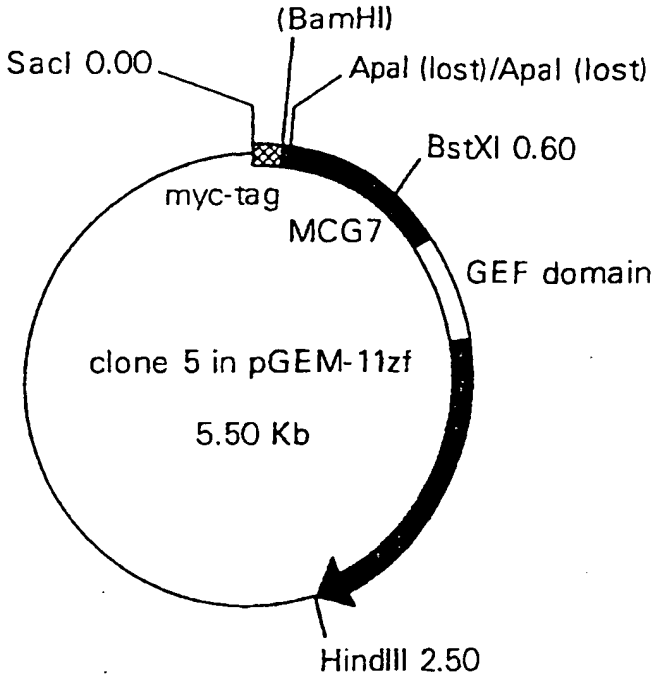
Plasmid name: clone 16 in pGEX-3X
Plasmid size:6.00 kb

FIGURE 18 (Cont. II)

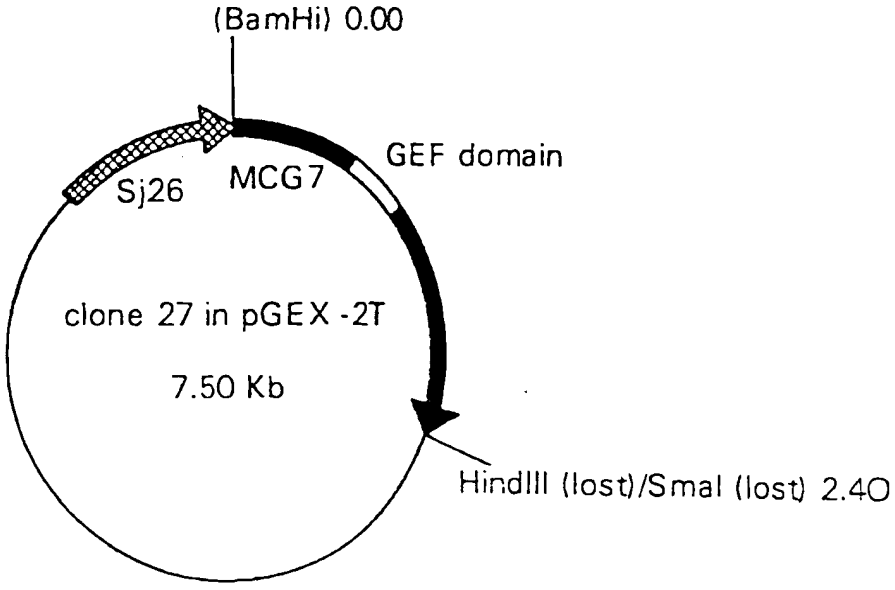


Plasmid name: clone 19 in pGEX-1
Plasmid size: 6.00 Kb

FIGURE 18 (Cont. III)



Plasmid name: clone 5 in pGEM-11zf
Plasmid size: 5.50 kb



Plasmid name: clone 27 in pGEX-2T
Plasmid size: 7.50 kb

FIGURE 18 (Cont. IV)

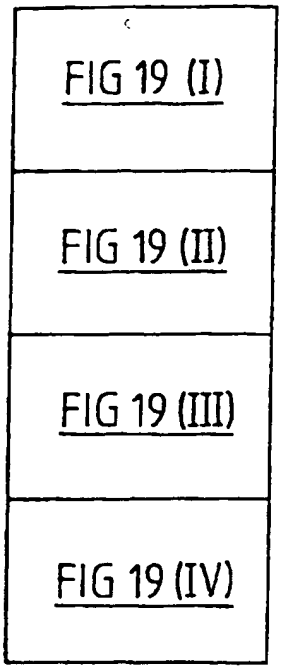


FIG 19

FIGURE 19 (I)

```
GCCCGCCGCC ATG CCG CCC TTA CTG CCC CTG CGC CTG TGC CGG      43
           Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg
            1               5                  10

CTG TGG CCC CGC AAC CCT CCC TCC CGG CTC CTC GGA GCG GCC      85
Leu Trp Pro Arg Asn Pro Pro Ser Arg Leu Leu Gly Ala Ala
             15                  20                  25

GCC GGG CAG CGG TCC AGA CCC AGT ACT TAT TAT GAA CTG TTG     127
Ala Gly Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu
                 30                  35

GGG GTG CAT CCT GGT GCC AGC ACT GAG GAA GTT AAA CGA GCT     169
Gly Val His Pro Gly Ala Ser Thr Glu Glu Val Lys Arg Ala
40                   45                  50

TTC TTC TCC AAG TCC AAA GAG CTG CAC CCA GAC CGG GAC CCT     211
Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp Pro
     55                  60                  65

GGG AAC CCA AGC CTG CAC AGC CGC TTT GTG GAG CTG AGC GAG     253
Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu
         70                  75                  80
```

FIGURE 19 (II)

```
GCA TAC CGT GTG CTC AGC CGT GAG CAG AGC CGC CGC AGC TAT        295
Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg Ser Tyr
                85                  90                  95

GAT GAC CAG CTC CGC TCA GGT AGT CCC CCA AAG TCT CCA CGA        337
Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg
                   100                 105

ACC ACA GTC CAT GAC AAG TCT GCC CAC CAA ACA CAC AGC TCC        379
Thr Thr Val His Asp Lys Ser Ala His Gln Thr His Ser Ser
110                 115                 120

TGG ACA CCC CCC AAC GCA CAG TAC TGG TCC CAG TTT CAC AGC        421
Trp Thr Pro Pro Asn Ala Gln Tyr Trp Ser Gln Phe His Ser
    125                 130                 135

GTG AGG CCA CAG GGG CCC CAG TTG AGG CAG CAG CAA CAC AAA        463
Val Arg Pro Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys
        140                 145                 150

CAA AAC AAA CAA GTG CTG GGG TAC TGC CTC CTC CTC ATG CTG        505
Gln Asn Lys Gln Val Leu Gly Tyr Cys Leu Leu Leu Met Leu
            155                 160                 165
```

FIGURE 19 (III)

```
GCG GGC ATG GGC CTG CAC TAC ATT GCC TTC AGG AAG GTG AAG        547
Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg Lys Val Lys
                170                 175

CAG ATG CAC CTT AAC TTC ATG GAT GAA AAG GAT CGG ATC ATC        589
Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile Ile
180                 185                 190

ACA GCC TTC TAC AAC GAA GCC CGG GCA CGG GCC AGG GCC AAC        631
Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg Ala Asn
    195                 200                 205

AGA GGC ATC CTT CAG CAG GAG CGA CAA CGG CTA GGG CAG CGG        673
Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg
        210                 215                 220

CAG CCG CCA CCA TCC GAG CCA ACC CAA GGC CCC GAG ATC GTG        715
Gln Pro Pro Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val
            225                 230                 235

CCC CGG GGC GCC GGC CCC TGA GGGGCTC ACCTGGATGG GGCCTGCAGT      763
Pro Arg Gly Ala Gly Pro   *
                240
```

FIGURE 19 (IV)

GCGTTCCCGC TTTGCTTCCT TCCCTGGACG GCCCGCTCCC CGAAACGCGC 813

GCAATAAAGT GATTCGCAG 832

FIGURE 20

>sp|P08622|DNAJ_ECOLI DNAJ PROTEIN >pir ||HHECDJ heat shock protein dnaJ -
Escherichia coli >gi |145769 (M12565)-heat shock protein dnaJ
[Escherichia coli] >gi |216441 (D10483) dnaJ protein
[Escherichia coli]
Length = 376
Score = 138 (63.7 bits), Expect = 1.2e-10, P = 1.2e-10
Identities = 25/62 (40%), Positives = 39/62 (62%)

```
Query: 35 YYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNPSLHSRFVELSEAYRVLSREQSRRS 94
          YYE+LGV    A    E+++A+    + + HPDR+ G+     ++F E+ EAY VL+  Q R +
Sbjct:  6 YYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAA 65
Query: 95 YD   96
          YD
Sbjct: 66 YD   67
```

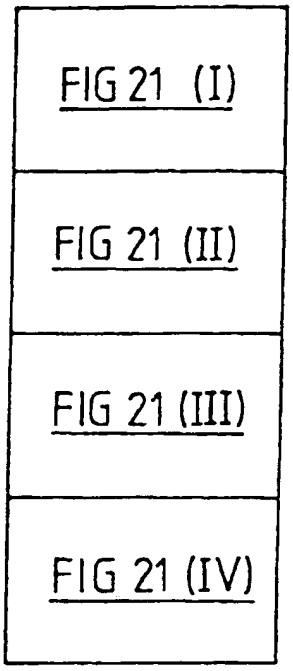


FIG 21

FIGURE 21 (I)

>gi|1703590 (U80439) contains similarity to a DNAJ-like domain (Caenorhabditis elegans]
Length = 345

Score = 98 (45.2 bits), Expect = 5.2e-12, Sum P(3) = 5.2e-12
Identities = 17/37 (45%), Positives = 28/37 (75%)

Query: 28 QRSRPSTYYELLGVHPGASTEEVKRAFFSKSKELHPD 64
++ R T+YE+LGV A+ E+K AF+++SK++HPD
Sbjct: 22 KKIRQRTHYEVLGVESTATLSEIKSAFYAQSKKVHPD 58

Score = 74 (34.1 bits), Expect: = 5.2e-12, Sum P(3) = 5.2e-12
Identities = 17/32 (53%), Positives = 19/32 (59%)

FIGURE 21 (II)

```
Query: 71 SLHSRFVELSEAYRVLSREQSRRSYDDQLRSG 102
          S  + F+EL  AY VL R   RR YD QLR G
Sbjct: 64 SATASFLELKNAYDVLRRPADRRLYDYQLRGG 95

Score = 39 (18.0 bits), Expect = 5.2e-12, Sum P(3) = 5.2e-12
Identities = 10/42 (23%), Positives = 19/42 (45%)

Query: 162 LLMLAGMGLHYIAFRKVKQMHLNFMDEKDRIITAFYNEARAR 203
           L+++AG    Y+       Q L+  + ++D I   F  +   R
Sbjct: 158 LVLVAGYNGGYLYLLAYNQKQLDKLIDEDEIAKCFLRQKEFR 199
```

FIGURE 21 (III)

```
>gnl |PID |e281266 (Z81030) C01G10.12 [Caenorhabditis elegans]
          Length = 191

 Score = 96 (44.3 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
 Identities = 17/41 (41%), Positives = 27/41 (65%)

Query: 35 YYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNPSLHSR 75
           YYE++GV   A+ +E++ AF  K+K+LHPD+    +    SR
Sbjct: 19 YYEIIGVSASATRQEIRDAFLKKTKQLHPDQSRKSSKSDSR 59

 Score = 54 (24.9 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
 Identities = 10/22 (45%), Positives = 15/22 (68%)

Query: 75 RFVELSEAYRVLSREQSRRSYD 96
           +F+ + EAY VL  E+ R+ YD
```

FIGURE 21 (IV)

```
Sbjct: 71 QFMLVKEAYDVLRNEEKRKEYD 92

Score = 35 (16.1 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
Identities = 9/44 (20%), Positives = 22/44 (50%)

Query: 141 QGPQLRQQQHKQNKQVLGYCLLLMLAGMGLHYIAFRKVKQMHLN 184
           + P+    + KQ  ++L       ++A +G + +  RK++   L+
Sbjct: 145 RNPEDEYLREKQKNRMLVVLAATVMALIGANIVYIRKLQADRLS 188
```

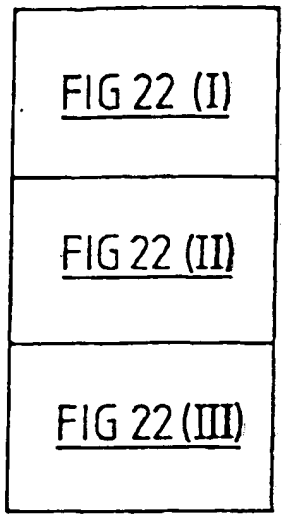


FIG 22

FIGURE 22 (I)

```
>sp|Q10209|YAY1_SCHPO HYPOTHETICAL 44.8 KD PROTEIN C4H3.01 IN
CHROMOSOME I
          >gi|1184014 (Z69380) unknown [Schizosaccharomyces pombe]
          Length = 392

Score = 84 (38.8 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 13/36 (36%), Positives = 25,36 (69%)

Query: 35 YYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNP 70
          YY+LLG+   A+  ++K+A+   + + HPD++P +P
Sbjct: 9  YYDLLGISTDATAVDIKKAYRKLAVKYHPDKNPDDP 44

Score = 64 (29.5 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 14/40 (35%), Positives = 23/40 (57%)
```

FIGURE 22 (II)

```
Query: 75 RFVELSEAYRVLSREQSRRSYDDQLRSGSPPKSPRTTVHD 114
          +F ++SEAY+VL  E+ R  YD   +  + P+   T  +D
Sbjct: 50 KFQKISEAYQVLGDEKLRSQYDQFGKEKAVPEQGFTDAYD 89

Score = 37 (17.1 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 9/29 (31%), Positives = 15/29 (51%)

Query: 190 DRIITAFYNEARARARANRGILQQERQRL 218
           DR   A   E  A A+  + +++  RQR+
Sbjct: 149 DRKKNAQIREREALAKREQEMIEDRRQRI 177

Score = 33 (15.2 bits), Expect = 0.00081, Sum P(3) = 0.00081

Identities = 8/19 (42%), Positives = 11/19 (57%)
```

FIGURE 22 (III)

```
Query: 140  PQGPQLRQQQHKQNKQVLG 158
            PQG    + Q+   +   QVLG
Sbjct: 44   PQGASEKFQKISEAYQVLG 62
```

FIGURE 23

```
>gnl|PID|e253406 (X77635) tumorous imaginal discs [Drosophila virilis]
        >gnl|PID|e263866 (Y07700) Tid58 protein [Drosophila virilis]
        Length = 529

 Score = 153 (70.6 bits), Expect = 9.7e-13, P = 9.7e-13
 Identities = 27/71 (38%), Positives = 44/71 (61%)

Query: 26
    AGQRSRPSTYYELLGVHPGASTEEVKRAFFSKSKELHPDRDPGNPSLHSRFVELSEAYRV 85
    +   R +    YY   LGV    A+ +++K+A++   +K+ HPD +   +P     +F ++SEAY V
Sbjct: 72
    SSSRMQAKDYYATLGVAKNANAKDIKKAYYELAKKYHPDTNKDDPDASKKFQDVSEAYEV 131

Query: 86 LSREQSRRSYD 96
           LS +Q RR YD
Sbjct:132 LSDDQKRREYD 142
```

FIG 24 (I)

FIG 24 (II)

FIG 24 (III)

FIG 24

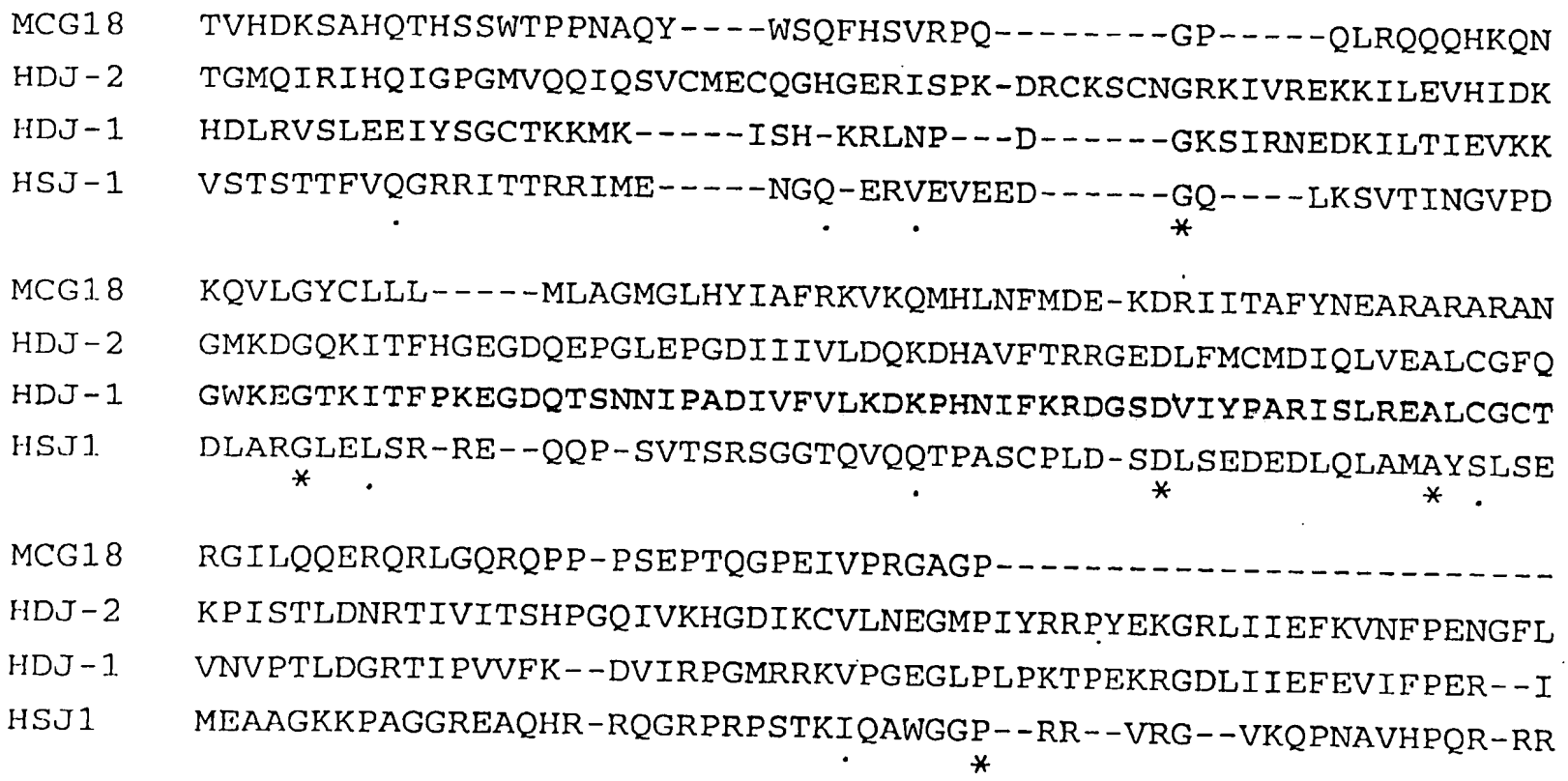
FIGURE 24(I)

```
MCG18   ---------------------MPPLLPLRLCRLWP-RN--PP-----------SRLLGAA
HDJ-2   MVKETTYYDVLGVKPNATQEELKKAYRKLALKYHPDKN--PN----EGEKFKQISQAYEV
HDJ-1   MGKD--YYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPG----AEEKFKEIAEAYDV
HSJ1    M-AS--YYEILDVPRSASADDIKKAYRRKALQWHPDKN--PDNKEFAEKKFKEVAEAYEV
                             .         .  * .*  *

MCG18   AGQRSRPSTY--YELLGVH-------------PGA------------ST-EEVKRAFFS-
HDJ-2   LSDAKKRELYDKGGEQAIK---------EGGAGGG----------FGSPMDIFDMFFGGG
HDJ-1   LSDPRKREIFDRYGEEGLKGSGP-----SGGSGGGANGTSFSYTFHGDPHAMFAEFFG--
HSJ1    LSDKHKREIYDRYGREGLTGTGTGPSRAEAGSGGP--G--FTFT-FRSPEEVFREFFG--
              .   .       .               *                 .   **

MCG18   KSKELHPDRDPGNP----SLHSRFVELSEAYRVLSREQSRRS--YDDQLRSGSPPKSPRT
HDJ-2   GRMQRERRGKNVVHQLSVTLEDLYNGATRKLALQKNVICDKCEGRGGKKGAVECCPNCRG
HDJ-1   GRNPFDTFFGQRNGEEGMDIDDPFSGFPMGMGGFTNVNFGRS--RSAQEPARKKQDPPVT
HSJ1    SGDPFAELFDDLGP--FSELQNRGSRHSGPFFTFSSSFPGHSDFSSSSFSFSPGAGAFRS
                            .                    ..
```

FIGURE 24 (II)



PCT/AU98/00380

09/424458

FIGURE 24 (III)

```
MCG18    ------------------------------------------------------------
HDJ-2    SPDKLSLLEKLLPERKEVEETDEMDQVELVDFDPNQERRRHYNGEAYEDDEHHPRGGVQC
HDJ-1    PQTSRTVLEQVLPI
HSJ1     PLAASSSEHRAQPD---------LIQILTGGSDSLWEEKRGVS----------------

MCG18    ---
HDJ-2    QTS
HDJ-1    ---
HSJ1     ---
```

* = amino acid identity in all 4 proteins

\- = conservative substitution

CT/AU98/00380

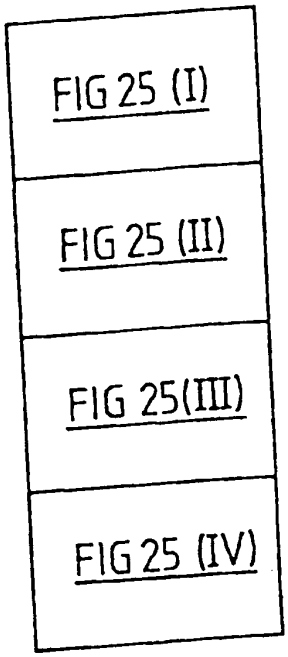


FIG 25

FIGURE 25 (I)

```
CAAGGAGCCT CTGCCTGCCC GTCGTCGTC ATG CCG TCC CTG TTG CTC      47
                                Met Pro Ser Leu Leu Leu
                                 1               5

CAG CTG CCC CTG CGC CTA TGC CGG CTG TGG CCG CAT AGC CTT      89
Gln Leu Pro Leu Arg Leu Cys Arg Leu Trp Pro His Ser Leu
            10                  15                  20

TCC ATC CGA CTT CTC ACA GCC GCC ACA GGG CAG CGG TCT GTC     131
Ser Ile Arg Leu Leu Thr Ala Ala Thr Gly Gln Arg Ser Val
                25                  30

CCT ACT AAT TAC TAT GAA TTG TTG GGC GTG CAT CCG GGT GCC     173
Pro Thr Asn Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala
 35                  40                  45

AGC GCT GAA GAG ATT AAA CGT GCT TTT TTC ACC AAG TCA AAA     215
Ser Ala Glu Glu Ile Lys Arg Ala Phe Phe Thr Lys Ser Lys
     50                  55                  60

GAG CTA CAC CCT GAT CGA GAC CCT GGG AAC CCA GCC CTG CAT     257
Glu Leu His Pro Asp Arg Asp Pro Gly Asn Pro Ala Leu His
         65                  70                  75
```

FIGURE 25 (II)

```
AGC CGC TTT GTG GAG CTG AAT GAG GCA TAT CGA GTG CTC AGT      299
Ser Arg Phe Val Glu Leu Asn Glu Ala Tyr Arg Val Leu Ser
             80                  85                  90

CGT GAG GAA AGT CGT CGT AAC TAT GAC CAC CAG CTG CAT TCA      341
Arg Glu Glu Ser Arg Arg Asn Tyr Asp His Gln Leu His Ser
                 95                 100

GCC AGT CCT CCA AAG TCT TCA GGG AGC ACA GCC GAG CCT AAG      383
Ala Ser Pro Pro Lys Ser Ser Gly Ser Thr Ala Glu Pro Lys
105                 110                 115

TAT ACG CAA CAG ACA CAC AGC AGC TCC TGG GAA CCC CCC AAC      425
Tyr Thr Gln Gln Thr His Ser Ser Ser Trp Glu Pro Pro Asn
    120                 125                 130

GCT CAA TAC TGG GCC CAG TTC CAC AGT GTG AGG CCG CAG GGG      467
Ala Gln Tyr Trp Ala Gln Phe His Ser Val Arg Pro Gln Gly
        135                 140                 145
CCG GAG TCA AGG AAG CAG CAG CGT AAA CAC AAC CAG CGG GTC      509
Pro Glu Ser Arg Lys Gln Gln Arg Lys His Asn Gln Arg Val
            150                 155                 160
```

FIGURE 25 (III)

```
CTG GGG TAC TGC CTC CTG CTC ATG GTG GCA GGC ATG GGC CTG      551
Leu Gly Tyr Cys Leu Leu Leu Met Val Ala Gly Met Gly Leu
                165                 170

CAC TAT GTT GCC TTC AGG AAG CTG GAG CAG GTG CAT CGC AGC      593
His Tyr Val Ala Phe Arg Lys Leu Glu Gln Val His Arg Ser
175                 180                 185

TTC ATG GAT GAA AAG GAC CGG ATC ATT ACA GCC ATC TAC AAT      635
Phe Met Asp Glu Lys Asp Arg Ile Ile Thr Ala Ile Tyr Asn
    190                 195                 200

GAC ACT CGG GCC AGG GCC AGG GCC AAC AGA GCC AGG ATT CAG      677
Asp Thr Arg Ala Arg Ala Arg Ala Asn Arg Ala Arg Ile Gln
        205                 210                 215

CAG GAG CGC CAC GAG AGG CAG CAG CCT CGG GCA GAA CCC TCC      719
Gln Glu Arg His Glu Arg Gln Gln Pro Arg Ala Glu Pro Ser
            220                 225                 230
```

FIGURE 25 (IV)

```
CTG CCT CCA GAA AGC TCC AGG ATC ATG CCC CAG GAC ACA AGC      761
Leu Pro Pro Glu Ser Ser Arg Ile Met Pro Gln Asp Thr Ser
                235                 240

CCC TGAGAGGCTT AACTAAATGG GACCTTCATT GGTCCTCTCC CTGCTGCCTG   814
Pro  *
245

TCCAGAACTA CACGTGCAAT AAACTCATTT TCAG (A)n                    849
```

FIGURE 26

```
human MCG18 MPPLL---PLRLCRLWPRNPPSRLLGAAAGQRSRPSTYYELLGVHPGASTEEVKRAFFSK
mouse MCG18 MPSLLLQLPLRLCRLWPHSLSIRLLTAATGQRSVPTNYYELLGVHPGASAEEIKRAFFTK
            **     *********.     *** **.**** *..************.**.*****.*

human MCG18 SKELHPDRDPGNPSLHSRFVELSEAYRVLSREQSRRSYDDQLRSGSPPKSPRTTVHDKSA
mouse MCG18 SKELHPDRDPGNPALHSRFVELNEAYRVLSREESRRNYDHQLHSASPPKSSGSTAEPKYT
            *************.******** *********.*** ** **.* *****   .*   * .

human MCG18 HQTHSS-WTPPNAQYWSQFHSVRPQGPQLRQQQHKQNKQVLGYCLLLMLAGMGLHYIAFR
mouse MCG18 QQTHSSSWEPPNAQYWAQFHSVRPQGPESRKQQRKHNQRVLGYCLLLMVAGMGLHYVAFR
            .***** * *******.**********. *.**.*.*..*********.*******.***

human MCG18 KVKQMHLNFMDEKDRIITAFYNEARARARANRGILQQERQRLGQRQPPPSEPTQGPE---
mouse MCG18 KLEQVHRSFMDEKDRIITAIYNDTRARARANRARIQQER---HERQQPRAEPSLPPESSR
            *. *.*  *********** **..********  .****    .** * .**.  **

human MCG18 IVPRGAGP
mouse MCG18 IMPQDTSP
            *.*.  . *
```

FIGURE 27

```
TTGA AGT CTA GCC CCA TCC TGG TCC AAT GCG CTC TTG GTA          40
  *  Ser Leu Ala Pro Ser Trp Ser Asn Ala Leu Leu Val
       1               5                  10
GCC TCC TTT CCC AGC TGC CCG CCC GCC GCC ATG CCG CCC TTA       82
Ala Ser Phe Pro Ser Cys Pro Pro Ala Ala Met Pro Pro Leu
         15                  20                  25

CTG CCC CTG CGC CTG TGC CGG CTG TGG CCC CGC AAC CC          120
Leu Pro Leu Arg Leu Cys Arg Leu Trp Pro Arg Asn Pro
            30                  35
```

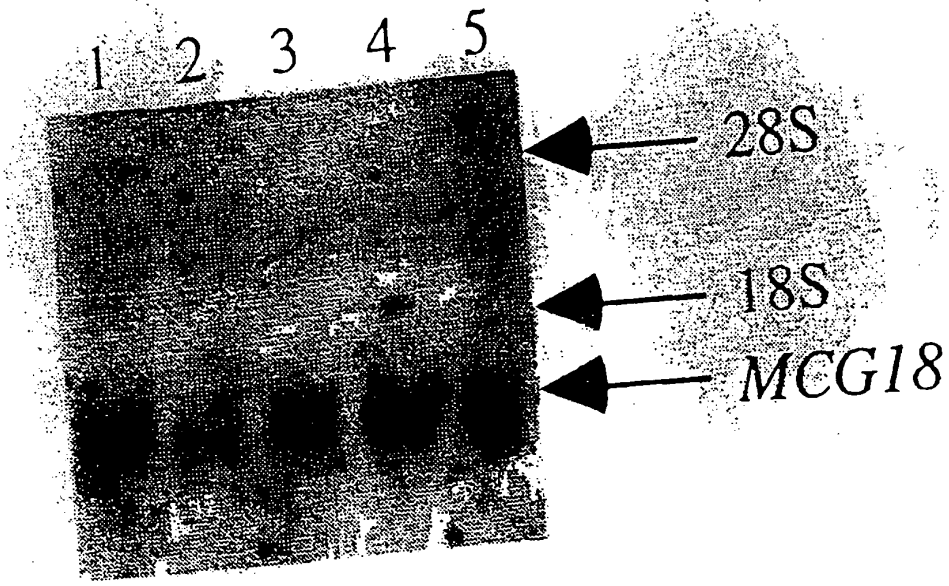


FIG 28